



```

1 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCGCTG
51 CGCCAGGATG GAGTTCGTGA AATGCCCTGG CCACCCCGAA GAGTTCCTACA
101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
151 GACCAGGACT CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA
201 TCAGACCACT CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA
251 TGCACAACGC AGTGTGCATA TTTTATCTGG TTCTCCGAGC TCTGGACACA
301 CTGGAAGATG ACATGACCAT CAGTGTGGAA AAGAAGGTCC CGCTGTTACA
351 CAACTTTCAC TCTTTCCTTT ACCAACCAGA CTGGCGGTTT ATGGAGAGCA
401 AGGAGAAGGA TCGCCAGGTG CTGGAGGACT TCCCAACGTA CTGCCACTAT
451 GTTGCTGGGC TGGTCGGAAT TGGCCTTTCC CGTCTTTTCT CAGCCTCAGA
501 GTTTGAAGAC CCCTTAGTTG GTGAAGATAC AGAACGTGCC AACTCTATGG
551 GCCTGTTTCT GCAGAAAACA AACATCATCC GTGACTATCT GGAAGACCAG
601 CAAGGAGGAA GAGAGTTCTG GCCTCAAGAG GTTTGGAGCA GGTATGTTAA
651 GAAGTTAGGG GATTTTGCCTA AGCCGGAGAA TATTGACTTG GCCGTGCAGT
701 GCCTGAATGA ACTTATAACC AATGCACTGC ACCACATCCC AGATGTCATC
751 ACCTACCTTT CGAGACTCAG AAACCAGAGT GTGTTTAACT TCTGTGCTAT
801 TCCACAGGTG ATGGCCATTG CCAC'TTTGGC TGCC'TGTTAT AATAACCAGC
851 AGGTGTTCAA AGGGGCAGTG AAGATTCGGA AAGGGCAAGC AGTGACCCCTC
901 ATGATGGATG CCACCAATAT GCCAGCTGTC AAAGCCATCA TATATCAGTA
951 TATGGAAGAG ATTTATCATA GAATCCCCGA CTCAGACCCA TCTTCTAGCA
1001 AAACAAGGCA GATCATCTCC ACCATCCGGA CGCAGAATCT TCCCAACTGT
1051 CAGCTGATTT CCCGAAGCCA CTACTCCCCC ATCTACCTGT CGTTTGTCTAT
1101 GCTTTTGGCT GCCCTGAGCT GGCAGTACCT GACCACTCTC TCCCAGGTAA
1151 CAGAAGACTA TGTTTCAGACT GGAGAACACT GATCCCAAAT TTGTCCATAG
1201 CTGAAGTCCA CCATAAAGTG GATTTACTTT TTTTCTTTAA GGATGGATGT
1251 TGTGTTCTCT TTATTTTCTT CCTACTACTT TAATCCCTAA AAGAACGCTG
1301 TGTGGCTGGG ACCTTTAGGA AAGTGAATG CAGGTGAGAA GAACCTAAAC
1351 ATGAAAGGAA AGGGTGCCCTC ATCCCAGCAA CCTGTCCTTG TGGGTGATGA
1401 TCACTGTGCT GCTTGGCGCT CATGGCAGAG CATTGAGTGC CACGGTTTAG
1451 GTGAAGTCGC TGCATATGTG ACTGTCATGA GATCCTACTT AGTATGATCC
1501 TGGCTAGAAAT GATAATTAAA AGTATTTAAT TTGAAAAAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1601 AAAAAA (SEQ ID NO:1)

```

#### FEATURES:

5'UTR: 1-57  
Start Codon: 58  
Stop Codon: 1180  
3'UTR: 1183

#### Homologous proteins:

##### Top 10 BLAST Hits

	Score	E
CRA 108000024649260 /altid=gi 12734163 /def=ref XP_005134.2  fa...	770	0.0
CRA 18000004925908 /altid=gi 4758350 /def=ref NP_004453.1  farn...	743	0.0
CRA 18000004929946 /altid=gi 2135096 /def=pir  I38245 farnesyl-...	741	0.0
CRA 18000004993865 /altid=gi 2136196 /def=pir  I52090 squalene ...	740	0.0
CRA 18000004932414 /altid=gi 6753838 /def=ref NP_034321.1  farn...	671	0.0
CRA 18000004937535 /altid=gi 9506591 /def=ref NP_062111.1  farn...	654	0.0
CRA 1000682330885 /altid=gi 6002565 /def=gb AAF00038.1  (AF0903...	582	e-165
CRA 335001098694081 /altid=gi 11514495 /def=pdb 1EZFA Chain A,...	579	e-164
CRA 18000005103884 /altid=gi 2463565 /def=dbj BAA22557.1  (AB00...	282	1e-74
CRA 18000005103885 /altid=gi 7434086 /def=pir  T00489 farnesyl-...	280	4e-74

FIGURE 1A

BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960...	1441	0.0
gi 12945082 /dataset=dbest /taxon=960...	1370	0.0
gi 12921315 /dataset=dbest /taxon=960...	1346	0.0
gi 11642571 /dataset=dbest /taxon=96...	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606...	1281	0.0
gi 13040072 /dataset=dbest /taxon=960...	1233	0.0
gi 12944143 /dataset=dbest /taxon=960...	1055	0.0

**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|12926380 placenta  
gi|12945082 T cells from T cell leukemia  
gi|12921315 Fetal brain  
gi|11642571pancreas  
gi|9141948 Burkitt lymphoma  
gi|13040072 bladder

From tissue screening panels:

Whole liver

FIGURE 1B

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMPPK MDQDSLSSSL KTCYKYLNQ  
51 SRSFAAVIQA LDGEMRNAVC IFYLVLRALD TLEDDMTISV EKKVPLLHNF  
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE  
151 DPLVGEDTER ANSMGLFLQK TNIIRDYLED QGGREFWPQ EVWSRYVKKL  
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPQ  
251 VMAIATLAAC YNNQVFKGA VKIRKGQAVT LMMDATNMPA VKAIIYQYME  
301 EIYHRIPDS PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL  
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2

1 48-51 NQTS  
2 239-242 NQSV

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 5

1 39-41 SLK  
2 50-52 TSR  
3 158-160 TER  
4 313-315 SSK  
5 322-324 TIR

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 3

1 81-84 TLED  
2 145-148 SASE  
3 147-150 SEFE

[4] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 2

1 137-142 GIGLSR  
2 276-281 GQAVTL

[5] PDOC00009 PS00009 AMIDATION  
Amidation site

22-25 GGKR

[6] PDOC00802 PS01044 SQUALEN\_PHYTOEN\_SYN\_1  
Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL

[7] PDOC00802 PS01045 SQUALEN\_PHYTOEN\_SYN\_2  
Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQGGREFWP

**Membrane spanning structure and domains:**

Helix	Begin	End	Score	Certainty
1	125	145	0.834	Putative
2	241	261	1.467	Certain
3	339	359	1.716	Certain

FIGURE 2B

**BLAST Alignment to Top Hit:**

```
>CRA|18000004925908 /altid=gi|4758350 /def=ref|NP_004453.1|
    farnesyl-diphosphate farnesyltransferase 1;
    Farnesyl-diphosphate farnesyltransferase 1 (squalene
    synthase); Squalene synthase [Homo sapiens] /org=Homo
    sapiens /taxon=9606 /dataset=nraa /length=417
    Length = 417

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA
Sbjct: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60

Query: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
          IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257
          KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRI PDS DPSSSKTR 317
          AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRI PDS DPSSSKTR
Sbjct: 301 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRI PDS DPSSSKTR 360

Query: 318 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLT TLSQVTE DYVQTGEH 374
          QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLT TLSQVTE DYVQTGEH
Sbjct: 361 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLT TLSQVTE DYVQTGEH 417 (SEQ ID
NO:4)

>CRA|108000024649260 /altid=gi|12734163 /def=ref|XP_005134.2|
    farnesyl-diphosphate farnesyltransferase 1 [Homo
    sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
    /length=431
    Length = 431

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA
Sbjct: 15 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 74

Query: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 75  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 134

Query: 121 VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 135 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194
```

FIGURE 2C

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV  
Sbjct: 195 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 254

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257  
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL  
Sbjct: 255 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 314

Query: 258 AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 315 AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 374

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 374  
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH  
Sbjct: 375 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 431 (SEQ ID NO:5)

>CRA|18000004929946 /altid=gi|2135096 /def=pir||I38245  
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21),  
hepatic - human /org=human /taxon=9606 /dataset=nraa  
/length=417  
Length = 417

Score = 741 bits (1893), Expect = 0.0  
Identities = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60  
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA  
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120  
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ  
Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137  
VLEDFPT YCHYVAGLVG  
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV  
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257  
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL  
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300

Query: 258 AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 301 AACYNQOVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 360

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 374  
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTSLQVTEDYVQTGEH  
Sbjct: 361 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTSLQVTEDYVQTGEH 417 (SEQ ID NO:6)

FIGURE 2D

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00494	1/2	47	126 ..	1	88 [.	124.6	1.1e-33
PF00494	2/2	127	291 ..	146	317 .]	301.1	1.3e-86

FIGURE 2E

1 TATTTATTCC TAATTAATG GGGAGGAAAG TCTTTGAAGA GGAACCTCTA  
51 CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTTT  
101 TGGGGTTCCC TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG  
151 GACTTAGGAT TTTTAGTTTA CAGTAGTAGG GGAAACACTC TGTAATCTAA  
201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC  
251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG  
301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA  
351 GTATCTGGGG GATAGTGCAG GAATAGTGAA CAGCTAGACA AAAAGTCCTA  
401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG  
451 GGTGGAAGGC TGCAGCCTCT CAGGATCCCT ATAGGTGCTT TGGCTTTTGT  
501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTTCC  
551 TGTTTGTTTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA  
601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT  
651 TCTCCTGCC T CAGCCTCCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA  
701 TGCCTGGCTA ATTTTGTAT TTTTAGTAGA GACGCAAGTT CAGCATGTTG  
751 GCCAGGCTGG TCTTGAACCT CAGACCTCAG GTGATCCGCC CGCCTTGGCC  
801 TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCTC GGCTAGACCT  
851 GACAGGTTTT AAAAGGATTA CTGGTTGCTG TGTTAAAACA GACTGCAGGA  
901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTTT TTTTGGAGAC GTAGTCTTGC  
951 TCTGTTGGCC TGGCTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC  
1001 TCCGCTTCCC GGGTTCAAGT GATTCTCCTG CCTCAGCCTC CGGAGTAGTT  
1051 GGGACTACAG GCGCCACCA CCACACTCGG CTTTTTTTGT TTTTGTAGT  
1101 AGACGGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT  
1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTT GCGATTACAG GCGTGAGCCA  
1201 CCACGCTG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA  
1251 TGAGAGAAGT TTCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAGCTCC  
1301 TTTTCTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGGCAGC  
1351 TGAAGCTCCA GGAGTGTGTG GGGCTCCCTG GGGCTGGATG GCGGTGGCGG  
1401 GCAGGCGAGC TGGGCTGTGC TCGGGTGTGT TACAGTAAAG ACGCCAGCT  
1451 TGGCGCTGGC CCGGCCTTTT CACGGTTTTA GGCTCTACAG AGAGCGGCTG  
1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGACG CGTGGGCGAC  
1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACTGCTCT CCCGACTGCG  
1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG  
1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG  
1701 CCGCGCAGC TCAGGGCACC AATCCCCTC GTCCGGCTCT TTCTCGGCCT  
1751 CCAATGAGCT TTAGGGTGT TATCAGCCA GTCTCCTTCC GCGACTGATT  
1801 GGCCGGGGTC TTCTAGTGT GAGCGGCCCT GGCCAATCAG GCGCCCGTCA  
1851 GCCCACCCCA CGAGGCCGCA GCTAGCCCCG CTGGCGGCCG AGGCCGGTTG  
1901 AAGTGGGCGG AGCGGCGGGC GGGGCGTCGC CGTACTAGGC CTGCCCCCTG  
1951 TCCGGCCAGC CCCTCGAAGC ACCTACTCCA CAGGTCCAGC CGGCCGGTGA  
2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCAGGAGT CCGCCGCTG  
2051 CGCCAGGATG GAGTTCGTGA AATGCCCTTG CCACCCGAA GAGTTCTACA  
2101 ACCTGGTGGC CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG  
2151 GACCAGGTGG GCGGAGCCTC CCTGCTTGCC CGGGGCGGGG AAGGAGCTCG  
2201 CTGGGCCGGC CTCAGGGCCT GAGCGGCCGG GCGCGATCT GGGCAAGGG  
2251 GCGCGGCGAG CAGGGCCGAC GCCTGGGTGT TCCCGTCCCC CTTTCCTCGA  
2301 GCCTTCCCC TGTAGGGCCC GGGTGGACGC GGCCGTCTG GCTGACCTGT  
2351 CCTGCCCTC GCAAGCCGCC CTGGGCATGA GCGACTTTTG CTGGTTTCCC  
2401 GGTGGTTGCG TCCCCGTTT CGTCCCCCTC GTGAGCATCG GCGCTTACCG  
2451 GTATTTTAA CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC  
2501 GGGAGAGGAC GAGTGAGTT TTTGGTAAGC GGAATGAACT ATGCAGATAA  
2551 CATCACATGA AGGCCGTTT TGGAATGAAG TCTGACTCCT CCAGTTTCAC  
2601 CACCTCTTCC GGAGCTCTCC CCGCCTTGCT GCCTTCCATC GCTTCATCCT  
2651 CGGTGCTTCC TGAGTTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT  
2701 GAGTTATCTA AGCTCTATG ATTAGCTAGG TGGTGTTGG AAGGTCAGAA  
2751 CTTGGTTTTA CTTAGATTTT TATCTGCCTC ATGCCTGTAC TATTTGTTTA  
2801 ATGAATGCAT AGGAGGTGTT TTTATTCCAA CAAGAAAATT ATTCTGACGC  
2851 GATTATTGAA TGAATAGACA AATTCAGCCA AGTTCTTCTG GTCTGGACCA  
2901 GCCTGGCTGA TTTCTGTAAC TTTTTTGGGC CAACAGGACA GTAGCAAATG  
2951 TGAATCAGGC CGAGGCTTGA TAGGTGCCTG AACATCGGAG TCTTCTTTC  
3001 AGTGTCATG TGCTTCAGTA AACACACTAG AAAATAAAT TCTGGTTTTT  
3051 GTCCCCAGTA GACTACACCC TCATTTGGTG TTATTTTTC ACGTGTATCT

FIGURE 3A



3101 TTAATACAGG TACATCCTTC AGTCTATTG TAGAACATTC AGTTTTCTTC  
3151 ATCTTTTCTT TGCCGGTGCT ACATTATTG AATTATTTG CTACAGAATA  
3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTATATT TAGATATAGC  
3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT  
3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT  
3351 TTATAAACT TACTTTTCTAG TGGAAGAGAG ACAATTTAAA AAAGCGAATG  
3401 TACAGTTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG  
3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCAATCCT  
3501 CTATGTCTCT TTCCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT  
3551 TGGTTTCTG TTTGGGAGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA  
3601 AAGACTTCAC AGTATACTGT TTTTGTACAT TTTGAGTTT TTTAAAAGCG  
3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT  
3701 AGTTGTAGTC TTTCTGGGCA GTTTTTACAT CCCCATGAGC CGTTAAAAAA  
3751 ATACCTGAAC CTTTAATTAG GGGAAATAAA TTGGAAAAAT ACATTTCCCT  
3801 TCACTTAACA TTACTTAGT TTCTCTTTT TTTTTTTTTT TTTTTTGAGA  
3851 TGGAGTCTTG CTCTGTTACC CAGGCTGGAG TGCAGTGGTG GCGGGACCTC  
3901 AGCTAGATGC AGCCTCCGCC TCCTGGGTTC AAGCAATTCT CCTGCCTCAG  
3951 CCTGCTGAGT AGCTGGGATT ACAGGCACCT GCCACTACGC CCGGCTGATT  
4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTC ACCATGTTGG CGAGGCTGGT  
4051 TTTGAACCTCT TGACCTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC  
4101 TAGGATTACA GCGCTGAGCC ACTGCACCCG GCCTTTTTTT TTTTTTTTTT  
4151 GAGGGGGGGG TCTCACTCCA TCGTCCAGCG TAGAATGCTG TGGCCTGAAC  
4201 ATGACTCACT CCAGTTTTGA CTTCTTGGC TGAAGCCATC CTCCCACCTC  
4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA  
4301 TGGCTAATTT TTAAATTTT TTGTAGACAC AATGTCTCGC TGCATTGCCC  
4351 AGGCTGGTCT TGAACCTCTG AGCTCAAGCG ATTTTCCAC CTCAGCCTTC  
4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCAACC AGTTTCTCTC  
4451 TGCAAAATAG GGAATAAAT TACGCTTAGC AGATATTGAG GGCTGATTAT  
4501 TTCTATCACA GAAGCATTTG GCTATAGAAT TTCAGGTTT AGTAACTTG  
4551 ATTTACACTG AATTTTTAGG TGCATATCAG TAAATCTACG GGCATATGCC  
4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC  
4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT  
4701 TATTTAGACT AATATCTTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA  
4751 TTAAGTTAGG TGAACAACCT TGGTAACTTA ACCTCTGAAC CACAGTACT  
4801 TCATCTGTAA AATAGGGATG TATGTATGGT AACGATTTT TAACCACAAC  
4851 TTCCCACTC TAAGATGGTC TGAAAAGAAT TTTTGTAGTG TTTGGCTCAG  
4901 AATCACTTGG CAGCAAAACC TGACTTGAAG TTGAGGCTTC ATTCATCCCA  
4951 CTTAGTATAT TCAAATGTTT TGCTAAAGAA ATAATTATGA GGTGCTACTT  
5001 CACACTGACT AGGGTTGTAT ATGCATTTA TTGCCTATTT TCTAAACAC  
5051 TAAAAATGCT AAATCTGCC CCAGGTCTTG CCACAGATGT TTCAGTGGAC  
5101 TATGGCCCTG TGAGACCTTA AAGGTTGAT TGAGTAAGGA TCACAGGTGA  
5151 TGTCCGCATT GTGCTTGCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA  
5201 TCAATCTGAT TATGTAAAT TATGTAAAT CAGTTCTCAA GTTTGTGGTT  
5251 TTTTCCCTT CCTGGAGAAA TCTATTCTAT TTTAAAGTGA GGAAGGCTCC  
5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTTAC TTGTGGAACT TTCAGCCTGA  
5351 GGCTGGAGCC CCTTCCTGGG AGTCTGGTCT TGTCGTCTTC CTGACCACCC  
5401 CCACACCTT CCTCTAAAT CCCTCCATCC CTGTTTTTCT CCCGCTTGCG  
5451 AGCTTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCAAGAG  
5501 GGACAGGCAC CAGTAGCCTG AGCTTGCTTT CTCCCCGGC TCATGGGAAT  
5551 CAAGCAGTAG AAATTTTTAG TGAGTGTGTT TTTCCATAGT ATGCTTACTA  
5601 GTTGTGTCTT CCTGTTTTGT TCTTGGTGAT TTGAAGAAAC CTGTTTACAA  
5651 GGTAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC  
5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT  
5751 GTATGGAAAAG GAGGGTAGT GTTCTTGAAG AGTGTGGGG TTTAAATCTA  
5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCCTGGCTTA ACATCACCCC  
5851 GAAACTGTTA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAAACA  
5901 CTTCTGCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG  
5951 AGCTCAGTCC AGAGCGGTA TTCTGTTTCT TTTACTCTGA AATCCTGCCT  
6001 CTCGATATTT TGAGAAGGAA GGAGTTGGTG AATTGTTTTA AAATCCTCGA  
6051 TGAATGCTT CATTTATTCA TGACACCACT TCTGAATATA TTTATGTGCC  
6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTTA  
6151 CTAATATTTT TTATGGCAAT AAAATGACTT TTTAGGATT ATGTGATTTA

FIGURE 3B

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

6201	AAAGATTGAC	CCTTTTGGCA	AAATACGTAT	TCATGATAGG	AAATATATAC
6251	AACATAGTTC	ACTTAAACCT	CCCACCAGAG	CCCAGGGTTC	ACTGTTACCA
6301	TTCTGAAGTG	ACTGGAATTT	CCTAGAAGTG	GATATGCCAT	ATTTTTTTAA
6351	CCACTCCTAT	TGGATATTTG	TTTTTTATTT	TTTTGAGATG	GGGTCCCACT
6401	CTGCAGTGTA	CAATATCATA	GTTCACTGTA	ACGTGTATCT	CTTGGGCTCA
6451	AGCGATCCTC	CCCACCTCAG	CCTCCCTGAG	TAGCTAGTCT	TCAGTAGCTA
6501	GACTATAGGT	GGGCGCCACC	ACAGCTGGCT	TTTTAAAAAA	TTTTTTATGA
6551	ACACGAGGTC	TCACTATGTT	GCCCAGGCTG	CCCTCAAAC	CCTGGGCTCA
6601	AGTGATTCTC	CCACCTTGGC	CTTCCGAAGT	GCAGGGATTA	TAGGCGTGCG
6651	CCACTGCACC	CGGCCCTGTT	GGATAAATGA	TTCCAGTCTC	TCCCAAAAAG
6701	AACTGTTGTA	AGACTGTGGG	GTGAGGGGAG	GGAAGGGACA	AATAGGAACC
6751	CGCCGTATTT	TCCACTCCCT	GTGGGCCTAA	AACTGCTCTA	AAAAATAGTC
6801	CATGAAAAAA	TACATAGTAC	AAACAGCAAC	TCTTTCTGAT	ATGCTTGCAT
6851	TTAAAATCAG	GCTTTTCTC	CCTTTTGGAA	AAACACAGTC	CTTGTTTGCT
6901	TTAGGGAAGA	GTAAAGGTCA	GTGCGTGCA	TTGCATTAAT	TTCAAGGGA
6951	AAGATGAGAA	GACATCTTGA	AAGGAATGGC	TGGCTTTCTA	GAGAATAGTA
7001	GAGGCTTAAT	AGGTGTCATA	GAAAAACCAG	GGTTGGACAG	TGGTAGTAAA
7051	ACGGCAAAAC	AGATTTTATT	CAGAAAAACT	ACTGCAGTAA	GAGGAGAGAG
7101	ACCTCGGTAC	AGAAGTCTC	CACTGCGAAT	ACAAAGAAAA	GTAGGAATTG
7151	ATGGCGGGGG	AGCCGGATGT	CAGTGGATGG	AAAATTATTA	CGAGGAAACA
7201	CAGGGGTGTG	CATTCTTGCT	GAAGGCAGGC	CAGAGTTATC	AGACATCACC
7251	TGAGGGATGG	AGGGGGATGT	GGAACCTAAT	CGGCTGTCTA	GGGTGATCAG
7301	ATACTGAAGT	TGGGGGATTC	TGGTCAAATC	AATTTAGCAG	GATTCTTGGT
7351	AAAAGTGGGC	GATGCAAAGA	CAGATGCGTT	GAGTACAAAG	TCCAGGCTTT
7401	ATTGGGAAGA	GGATTTACGC	GGAGCCCGAG	TAGAGTTTGG	TCTAGGGAGA
7451	CTCTGTCACT	GGGAGGACGA	GCGAGCCGCT	CGGAAGTGCG	CTGGGTCTCT
7501	TTAGCGGCCA	GTGGGTCTCG	GTGAGAAGGG	CAACAGCGGG	AGGAGGCGCC
7551	GGTGCGGAGC	GGGAGGCCGG	GGGCGGGGCT	GCGGGGCTGC	GGGGCGGGCC
7601	CGTTGTGGGT	CGGCCACGCG	CGTATTCGAG	TAGAGGGCGA	GCCCCGTCCCG
7651	CCTCTCGTCG	GGCGCTTCCC	AGATCTGCTT	GAGTCTATGG	AGGAAAAACT
7701	CCGCGGGGTC	CGCGATTCCC	ATGGCCGCG	CCGCCTGCGG	CACCAAGGCC
7751	ATGGCCCTCT	TCAAGCGCAC	CTTGGTGCTG	AGTCCCGCCG	CGGCGCCAG
7801	GGGCCCCGGC	GCAGGCACCG	CCCCGCGGGG	CTGCTGCTTG	CCTCCTGCCG
7851	CCTGGCCCTG	CAAGGACTGG	CCTCGGGGAG	AGGGCGGCAG	GCTGTGGAGC
7901	CGCCTGCCCC	AGTCCCAGTC	CCACTCCCAC	TCCCCTCCC	ACTCCCCTC
7951	CTGCTCCTCG	ACGTCTCCCA	CCGCCGTGTG	TGTTGTCTGC	CCGCAGGACT
8001	CGCTCAGCAG	CAGCCTGAAA	ACTTGCTACA	AGTATCTCAA	TCAGACCAGT
8051	CGCAGTTTCG	CAGCTGTTAT	CCAGGCGCTG	GATGGGAAAA	TGCGGTGAGT
8101	GATGGAGGCA	GCGCCTCTGG	CTTGGAGGAA	AGCTTGTCGG	GGACTTTTGA
8151	GTGTGTTGGA	AGCTACCTTT	TGATATAGCG	CTCAGCGTTG	CAGCCTCGTT
8201	GCTGTGGCTT	ATCCAGAACA	TAGCCCGGCC	CTACGTGTTT	ACTTTAGAAA
8251	GCCCTTCCAG	GCTCTTTGCC	ATCTAGTAGA	GTCCCTGCGG	GCCCAGCCTT
8301	TCAGAGAAGG	GGGGGGAGGG	GGTGATGTTT	ATTAACTTT	TTTAGTCTTG
8351	GCAGCTGAAC	CTGCCGTGTA	GCAGGTCGTG	TATTTCTCGG	CTTCCCTTAT
8401	CCAACCTTGC	ATTTCTATTT	CTAGCATATT	GGGTTGATTC	TTTTGAAGCT
8451	GCCTCTGTGC	ACATTACACC	CATGAACCTA	GACCAGTTGC	CTTTATGTAT
8501	GATCGTATTT	ATACTGAGAA	GTTACTGTGT	TTTTTGACTT	TCTTTTCTAT
8551	TTGCTACATA	TTAGTTCGGT	CTAAACGTTT	GGTCTTCTGG	TCTCCATAGT
8601	TCTACATTGG	TTAAATGCAA	CTCACTTCTG	GGAGTAGTGG	TGACATTCAA
8651	CTAGTAGGCT	TTTTAATAAA	CTACAGAAGT	TCATTACTCT	CATGTAAGGA
8701	AGGAAAACTA	ATGTAACCTT	CGTTAAGTAT	GAAAAGCGTT	GGATATCCTT
8751	ATAGTTCTTT	AGAGTTAAGG	GTGAGATGGG	TTTAGAAAAGT	GGCCAGGCAC
8801	AAGTTATTTT	AAAATAAAAA	ATCTTTGGCT	GTTTGTTCCT	ATATATTAAT
8851	AGTTTTCCTT	TTTTTACAGC	AACGCAAGTG	GCATATTTTA	TCTGGTTCTC
8901	CGAGCTCTGG	ACACACTGGA	AGATGACATG	ACCATCAGTG	TGGAAAAGAA
8951	GGTCCCGCTG	TTACACAAC	TTCACTCTTT	CCTTTACCAA	CCAGACTGGC
9001	GGTTCATGGA	GAGCAAGGAG	AAGGATCGCC	AGGTGCTGGA	GGACTTCCCA
9051	ACGGTGAGTG	GGGTTACGCA	TCTTGTCTAC	GGACTGTGTG	GTTCATAATT
9101	GCTAACGTGG	TTGTCCGGTA	GCCTCCATAC	ATGTGGAGAA	AGGTTAAATA
9151	AGCATTCTGA	GGGCAGCATA	ATGTGAGGGT	TAAAACTCC	GGTAGCCAAG
9201	ACTCTGAAGC	CAGGCTGCCT	GGGTGGAAT	CTCAAATCTC	CCACTTACTA
9251	AACTGTTGGT	TACTTACAAA	GACTCTCTGT	GCCTCAGTTT	CTTCATCTGT

FIGURE 3C

9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA  
9351 GAATTAACGT AGGTAATGCT CTTAGAAATGT TAGCTACTGC TGTTATTATC  
9401 AGTATTGGAA GTCCAGTGTT TCTTCCTGTG GGAAGACGCA GTCAAATTTT  
9451 AGTGTGTGA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT  
9501 GATGCAGCCT ACCTGTAACA CTGCTGGCCT CTTGACTACC CGGAGCCTGG  
9551 TAGCATGGGA CTGCTGCTCA CGATGGGCAG CAGCCTGGCA TGGGGGCGGT  
9601 GTCTGTTGGC AGCTAGGGCG AGCCTCTGCC ACTTCACCTG TGATCCTGGG  
9651 CAAGTTCCTT ATCTGCTTTG TGTCTCCGTC TCCTCGTTTG TAAAGTTAGA  
9701 GCTGAGAGGA TTAATTTTCGC ACATATAAAG TACTTAGTGC CTGGTACAGG  
9751 GTAAGTATTC TGTAAGTATT AGCTATTTGG TCTATTTTGT TGGAGTAAAG  
9801 TGGGTTATAG TTAATAATCCT AAGATTTTGA AAGTCCCTCA AGTTCACGTG  
9851 GACATCTGCC TAGGTCCTAC TATCCTAGAA TTCGCATGTC TTATCACACA  
9901 AATAACTGAT TCTTCCATAT CTTATAAATA AAGGTTTGAT TTAGCAAAGT  
9951 CACATGTTGT GTAATAGCTC GAAGAAGCCC TTTTGTCCA CAGTTGCCAG  
10001 AGCTTTTGGG GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC  
10051 TGAGTTGGGA GGGAGCTAAG TGGACAGAGA GTCCTCCACC CAAACAAAAG  
10101 AATCTTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAA AAAAAAAAAA  
10151 AAAAAAAAAA GGAATGTTTG GGAAGACTC TTGCGGTGCA AAGGCTGTTT  
10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAT ATAGTACAAC  
10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAATTCGA GTTTATACAG  
10301 TACAATCAA AGCAAGAAA AAAATTTATG ACGACTAGCT GGGTGAGAAT  
10351 TAGAATGCTA ACCCTGGGAA GGTCTGTGTG ATTTGACTCT CACAGGACAC  
10401 CTGATGACCA GAGGATGGGT TTCCTTTGAT GGGAAATCTG TGGCGATTCA  
10451 TTGATGGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCCAT  
10501 TTATAATGGA AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT  
10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA  
10601 TAATAATTAA AAAATTTCTG GGGCATGGGA TAAATGTGTT AGGTATTGCT  
10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG  
10701 TGTGAATGCT AACATAAATT TGGGGAATAT CGCCGTCAGA TTTCCAGATG  
10751 ATATTCCAAC ATGTTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT  
10801 GTTCCAGTGG AAAAATAATG CTTAGTTCTG GAAGGTTTCA GATGTGAACA  
10851 CTGAACCTCAT CGTTTTCTTT TTTGGGTAGT AGAGTTAGAG ATTCCATCCT  
10901 CTTGAAAGCA CAGTTGCCCC GGAAGAGTA AAAGGGAGCA GAAGGCGTAA  
10951 GCCAGGCACG GCTGTTTTCA CTGTTGTTCA CCTTTTGTAT CCTTACGAAT  
11001 ATGAAGATGT ACTAAGTTGT GTGTTTTGCG TGCATATATA ATTTTAAGCT  
11051 ACTTGAGTTG TAGGTCCCTC CAGTCTGTGA TTCAGTTTGA GATGGGACTG  
11101 TATGGGAATT AACAGTGCCT TGTCTTCTTA AGCAGTGATT TGTGTATGTG  
11151 CTGATATAGC TCAGTATGTC TTTGAAACCA GTTGTCTGGG GCTAGGCTGT  
11201 CAATCAGCTT TTGGCTAAGA GGTCCCAGGA TGGAACAAGT AGTGTGAAAG  
11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGGCAA  
11301 GTGAACTCC TCACCTCAGA GTGCCCCATT CTAGGCCCCC TCACTCCCAA  
11351 AGGGGTGAGG GATCACTGGG GCCATGGGAA TGTGCTTGTG CAGCTCTCGT  
11401 GGGCTCTCCT TCTGTACCAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA  
11451 ATCCCTGAGC CCACGTCTGC GTCCGCACAG TCTATTTCTC AAGGTCAGTC  
11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGACTGTGCC CTTGGGCTGT  
11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTGGATGG ATCCTGGCAC  
11601 CGAGGGCTGG GATATCCTCT CAAATGAATG TGAGGTGCCT CCCAGTGCTG  
11651 GAGAGAGCGG GATTCAGGAA GCAGTGGAAG GGAAGAGCCT GGGATATGGG  
11701 GATCAGCTGT CTGTGCCCTG CTGCATTCTG GAATAAAACT CTGAGGGACT  
11751 AAGAATTCTA AATTCAAACC TGAATCAACC AGGTGTTTAC AAAGATAAGT  
11801 TTGTCAAGTC AGGAGGATAC AATATATTTT ACTTAAGTTA CTAGCTCGAT  
11851 TGATCATTTT TAAATTTTGA GCTACATATA GTATGTGGGC CTCCATTGTG  
11901 CCTCTTATCC CAGGCCTTGC AGAATTTAGG AATAAGCCTC AATACAGTGT  
11951 TCTAACCAG TGACTTCCGC CTCGATGTAC AGTAGATTGA ACCTGATCCT  
12001 TTATACTTTA GTGATCATTA GTTGATACCA GTTCAAGTCA GGCTTTCTAG  
12051 AAATCTCATT GTATGTTAGG GGTTCGATTA GAGTACAGTC ATGCATCACT  
12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT  
12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT  
12201 AGCTACTACA GACGTAGGCT CTGTGGTACA GGCCATTGCT CCAAGGCTGC  
12251 ACATCTCTAC AGGATGGTAC TGTACTGAAT ACTGTAGGCA ATTGGAGCAC  
12301 AGTGGTAAAG ATTTGTGTAT TTAAACATAG AAAAGGTATA GTAAAAACAG  
12351 GGTGTTACAG TCTTAAGGCG CCACCATTGT ATTTCCAGTC TCCGTTGACT

FIGURE 3D

12401 GAAACATCAT TATACAGTAC ATGAGCACGT ATCTTTCTCA CCTGGTACTA  
12451 GTGGAAAGCT AGAAGGCTTA GAAGTCTACC TGTAACATA GCTTAAGTAA  
12501 TAATACAGCC TTATTTTAA ATGATAATAG CAATAATAGT GTTCACTTAT  
12551 TGAGCATTCT ACTATGAGTT ACTTACTAAA TATATTTTCA CGTTAATTTA  
12601 CTCTTTGTGT TATTTGATCT ATAACATCGT TTAACAGGGA AATTACCTAG  
12651 TACATAATGT ACTGTTATCT ACATTTTATC TAGATGAGGA AACTGAGGCA  
12701 CAGAGAAATT AAGTACTTTG CCTAGGATTA CCCGTGAAGT TAAGTGACAG  
12751 AATCAATGAA TCTGGAAGGT CTGGCTTACC ATCTCTTGTG CTGAGTCACT  
12801 CGCATACTTT ACTACCTCTA AGGTTTCTAA TCAGAGGAAT TTGTATCTGT  
12851 ATTCCCTGCT ACTCTTACCC TCTATGTGGG ATTTGGCCTT TCTCCATTAT  
12901 CCCTGTGAAC TCGCTCTGGG ACCTTCCTTC TTGTACTTGG AACCATCAGA  
12951 AAGTGATCTG AGAACATAGA AATCTACTGT GTTGTGAAAC AGAATTACCT  
13001 GGAAGCGGAA AAAGCCCTCC TGGCTCAATT CACATGTCAC GGCTTATGGT  
13051 CGTATCCGGG GAACATATGA AACTGGGCAC TGAGTGCGGA GTCAGGAAAG  
13101 CCCTGTCCAT TCTGGGGTTC TCTGGGGAAA ACGTGGACCC CTTCAATGTC  
13151 ACTTTCTCCT GTATATTTT GTTTTTACTT TTAGAAGTGT ACAATTACGT  
13201 AATAAATAAT AAAAAGTCGT TGGAAGGATA GGTGAAGTTC AGAAGTGAAA  
13251 GTGTTTTGGA GGAGTCTAAG CTCCTTCCCA CCCTCATTGA CTTTCCTCT  
13301 CTAATAAATA GAAGTGGTCT AACCAAGGAT CTGTGGAATG AGCAGAGTCC  
13351 AACGGAGATT CAGGGATTCT AATAACCTCT TGTAAGTCA CTGGTTTGTT  
13401 TCAGCCACAA GAAGGAATTA CCTTTTGACA TTGGCTTGAA CAGCTGTTGT  
13451 GCAAAGAAAA ACTTTTGA AAGTTCTGGA AGTACCAGAT TGATTTTATA  
13501 GGTTTTTTTT TTTTTTTT GAGGGACATG GGGGTATTGA CAGTTGATGT  
13551 TAATCAGAAA TCCTAAATTA TGTGTATTCC TGGTATGTG CAATCAGCCG  
13601 GCCACCTGGT TTTCTCTGG GCTCTTAATT TTAGGTGTAT TCCGAGGAAG  
13651 TTTTCTAAC TTTTCTGTAA ACACAGACCA GGTATATTGC ATACTTTCAA  
13701 TGTTTAACCA AATCTCTTCA CTGTTTGCAG TATTATCTGT AGGCTCTCAT  
13751 GTTTTAAGAC TTCCCATGG TGTTTTGTGA TTGTATTTG CTAACCTATA  
13801 AACAATTCTT TGAACCTAAA ACAAGATATT TGGGCAGTAA CAATAAATTT  
13851 TAAAAACATC AATTCAACTT TTTTACATTA GGGCTTGGAC TATGGAAAAA  
13901 GTATTGGGCA GCATGCCTCA TACTGAGTTG TTTAATGAAT TTTAAAGTAT  
13951 AGCCNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14001 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14051 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14101 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14151 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14201 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14251 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14301 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14351 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14401 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14451 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14501 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14551 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14601 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14651 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14701 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14751 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14801 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14851 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14901 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
14951 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15001 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15051 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15101 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15151 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15201 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15251 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15301 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15351 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15401 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN  
15451 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN

FIGURE 3E

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

15501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17551	NNNNNNNNNN	GGAGAGTCT	GTAGATGCT	GTTAGGTCG	CTTGGTCCAG
17601	AGCTGAGTTC	AAGTCCTGGA	TATCCTTGTT	AACCTTTTGT	CTTGTTGATC
17651	TATCTAATAT	TGACAGTGGG	ATGTTAGACT	CGCACACAAT	AATAATGAGA
17701	GACTTTAAGT	CTTTTTCTAG	GTCTCTAAGG	ACTTGCTTTA	TGAATCTGGG
17751	TGCTCCTGTA	TTGGGTACAT	ATATGTTTAA	GATAGTTAGC	TCTTCTTGTT
17801	GAATTGATCC	CTTTACCAT	ATGTAGTGGC	CTTCTTTGTC	TCTTTTGATC
17851	TTAGTTGGTT	TAAAGTCTGT	TTTATTAGAG	ACTAGGATTG	CATTCCCTGC
17901	TTTTTTTTTT	CGCTTGGTAG	ATCTTCCTCC	AGCTGTTTAT	TTTGAGCCTA
17951	TGTGCATCTC	TGCACGTGAG	ACGGGTCTCC	TGAATACAGC	ACAGTGACGG
18001	GCCTTGACTG	TTTATCCAAT	TTGCCAGTCT	GCGTCTTTTA	ACTGGGGCAT
18051	TTAGCCCACT	TATATTTAAG	GTTAATATTG	TTATGTTTGA	ATTTGATCTG
18101	TCATTATGAT	GTTTGCTGGT	TATTTTGCCC	ATTAATTGAT	GCAGTTTCTT
18151	CCTAGCCTCG	ATGGTCTTTA	CAATTTGGCA	TGTTTTTGCA	GTGGCTGGTA
18201	CCAGTTGTTT	CTTCCATT	TTACTGCTTC	CTTCAGGAGC	TCTTTTAGGG
18251	CAGGCCTGGT	GGTGACAAAA	TCTCTGAGCA	TTTGCTTGTC	TGTGAAGGAT
18301	TTTATTTCTC	CTTCACTTGT	GAACTTAGT	TTGGCTGGTT	ATGAGATTCT
18351	GGGTTGAAAA	TTCTTTAAGA	ATGCTGAATA	TTGGCCCCCA	CTCTCTTCTG
18401	GCTTGTAGGG	TTTCTGCTGA	GAGATCTGCT	GTTAGTCTGA	TGGGCTTCCC
18451	TTTGTGGGTA	ACCCGACCTT	TCTCTCTGGC	AGCCCTTAAC	ATTTTTTCCT
18501	TCATTTCAAC	GTTGGTGAAT	CTGACAATTA	CGTATCTTGG	GATTGCGCTT
18551	CTCGAGGAAT	GTCTTTGTGG	TGTTCTCTGT	ATTTCTTGAA	TTTGAATGTT

FIGURE 3F

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18601 GACCTGCCTT GCTAGGTTGG GGAAGTTCTC CTGGATAATA TACTGAAGAG
18651 TGTTTTGTAA CTTGGTTCCA TTCTGTCTAT CACTTTCAGG TACAACAATC
18701 ATAGCATTGG TCTTTTCACA TAGTCGCATA TTTATTGAAG CCTTTGTTCA
18751 TTTCTTTTCA TTCTTTTTC TCTAATCTTG TCTTCTTGCT TTATTTTCATT
18801 AATTTGATCT TCGATCACTG ATATCCTTTC TTCTGCTTGA TCGAATCGGC
18851 TATTGAAGCT TGTTTATGCT TTGTGAAATT CTTGTACTTT GGTTTTTCAGC
18901 TCCATCAGGT CATTTAAGCT CTTCTCTACA CTGGTTATTC TAGTTAGCCA
18951 TTTGTCCAAC CTTTTCTCAA GGTTTTAAGT TTCCTTGCGA TGGGTCAGAA
19001 CGTGCTGCTT TAGCTTGAG AGTTTTGTTA TTACCAACCT TCTGAAGCCT
19051 ACTTCTGTCA ACTCGTTAAA CTCATTGTCC ATCCAGTTTT GTTCCTTTGC
19101 TGGTGAGGAG TTACGTTCCCT TTGGAGGAGA AGAGGCGTTC TGTTTTTGGA
19151 ATTTTCAGCC TTTCTGCTGT GGTTTCTCCC CATCTTGTG GTTTTATCTA
19201 CCTTTGGTCT TTGATTTTGG TGACGTACAG ATGGGTTTTG GTGTGGGTGT
19251 CCTTTTGTG GATATTGATC CTATTCCTTT GTTTGTTAGT TTTCTTCTA
19301 ACAGAGGCCC GTCAGCTGCA GGTCTGTTGG AGTTGCTGGA GGTCCACTCT
19351 AGACCTGCTT TACCTGGGA TCACCAGTGG AGGCTGCAGA ACAGCAAATA
19401 TCGCGGCTG ATCCTTCCCTC TGGAAGCTTC GTCCAAGAAG GACACCCACC
19451 TATATGAGGT GTCTGTCGGC CCCTACTGGG AGGTGTCTCC TCCCAGTCAG
19501 GCTACATGGG GCTCAGGGAC CCACTTGAGG AGGCAGTCTG TCCGTTACTG
19551 GAGTTCAAAT GCCGAGCTGG GAGAACCACT GCTCTCTTCA GAGCTGTCAG
19601 GCAGGGATGT TTAAATCTGC AGAAGCCGTC TGCTGCCTTT TGTTTAGATA
19651 TGCCCTGCC CACAGATGC AATCTAGAGA GGCAGTAGGC CTTGCGGTGG
19701 GCTCCACCCA GTTCAAGCTT CTTGCTGCT TTGTTTACAC TGTGAGCATA
19751 GAAGTGCCTA CTGAAGCCTC AGCAATGGCG GGGAGGCGCT TCCCCTCACC
19801 AAGCTCCAGC ATCCCAGCTT GATCTCAGAC TGCTTGGCTA GCAGCAAGCA
19851 AGGTTCCATG GGCATGGGAC CCCCCGAGCC AGGCATGGA GGCAATCACC
19901 TGCTCTGCCA GTTGCGAAGA CTGGGAAAAG CACAGTATTT GGGCAGAGTA
19951 TACTGTTCTT CCAGGTACAG TCACTCACGC CTTTCTTGG CTAGGAAAGG
20001 GAAATCCCCT GACCCCTTGC ACTTCCTGGA TGAGGTGACG TCCTGCCCTG
20051 CTTTGGCTCA CCCTCCATGG GCTGCACCCA CTGTCCAACC AGTGCCAATG
20101 AGATGAACCA GGTACCTCAG TTGGAAATGC AGAAATCACC CATCTTCTGC
20151 ATCGATCTTG CTGGGAGCTG TAGACCAGAG CTGTTCTTAC TGGGGCATCT
20201 TGGAAGCAAC TCTGGGCTG AGTTTCTGTT TGTTGCCCTG ATGTATATCC
20251 CCAGTGCCTA GAATGATACT TGTTACATAG GAAGTGCTTG ATCCATGTTT
20301 GCACAAATGA ATCTTTCTCA TAATGAGGTT TCTCTAAACA AGCTGTTCTC
20351 CCAAAAACCT ACACCCAGCT TTATGTTGAA GCATCTCATT ATACATTGGA
20401 AAGATGAAAT GTGTAGTGAG ACTTTGAATC TTCTTTTGAA TCTAGAAACA
20451 TTAGCATTTT TAGACCATTC TATTTTAATA TTTATGAAAT TTATGAAATA
20501 ATAAGAAACA TGAGGCCGGG CTCAGTGGCT TATGCCTGTA ATCCCAGCAG
20551 TTTGGGAGGC CAGGGCTAGT GGATCATGAG GTCAGGAATT TGAGACCAGC
20601 TTGGCCAACA TGGTGAAACC CCACTTCTAC TAAAAATATA AAAATTAGCT
20651 GGGCGTGGT GTGCATGCCG GTAATGCCAG CTCCTGGAGA GGCTGAGGCA
20701 GGAGAATCAT TTGAACCTGG GAGGCGGAGT TTGCAGTGAG CTGAGATCGT
20751 GCCATTGCAC TCCAGCCTGG GCAACATTGC GAGACTCCAT CTCAAAAACA
20801 AAAACAAAAA CAAAAAAAT GTGTGACCTA AATTAGGCTT ATAGATGAAC
20851 CATTGCAGTC ATGATTAATT CCGCCATTGT TTGCCTTGTG ATCTTTGTG
20901 CCATGTCTGT ACATATTTCA TGATTTCTGT GTTTTACGG TTTCCATTTC
20951 AGATCTCCCT TGAGTTTAGA AATCTGGCTG AGAAATACCA AACAGTGATT
21001 GCCGACATTT GCCGGAGAAT GGGCATTGGG ATGGCAGAGT TTTTGGATAA
21051 GCATGTGACC TCTGAACAGG AGTGGGACAA GGTTAGTCTC ATAAAACAGT
21101 GTCTGTGTGT GATGTATTAG ACAGAGCTGG CAGTCTCAT AGTGAAGCTC
21151 AGAACAAGAA AAGTTGTCCA GTATTTTCTC CCCCTCTGGT TTTACAATTC
21201 ATCTGTTTAG GTTGAATGTC TCATCATAAA CAGTTTATTC CAGAGTTAAT
21251 TCCAAACCAG CAGCTATGTA GGATATCAGC CAGGCTAGGA GTAGGGTACT
21301 GGAGAGAAGT GCTTATCTAG ACAAAGGGAT GTAATTGACC ATGAAGATTA
21351 AAATAACACA TCAAAACATA AGGTAGGGTT AGGAGTCTTG CCTATTTTTC
21401 ATAGGAATGG TGTTTGTGAG ACTTACTCAT CACTTCTGTG GAAGTAAAGA
21451 CATTTTATTT ATTTATTTTA AAGCCAGTCA GATTTAGCAG GCAGAGACAT
21501 TTCAGACATC TAAAGTGTG ATGTATTTCA TACCTTTAAC TGTGCTTAAA
21551 TTAGGATCTC CGAAAAGATG CTGCTACATG GTCACTACGT TAGTGATAGT
21601 CCAAGTCTT GGGCCTCTTA ATTTTTCAAA CCTCAAACT TGACAGCAGT
21651 TATCTTTGGA ACTGCTGATT TGTGCTTCCT AAGTTAACAG CATACAATGA

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FIGURE 3G

21701 CTGCTAGAAA TCAATTTCTG CATTTAAGGT GAAGTTAGCC GGGTACTATG  
21751 GTTTACCTGT AATCTCAGCA CTTTGGGAGG CTGAGGTGGG AGGATCATTT  
21801 GAGCCCAGGA GTTAGACACA AGCCTAAGCA ACATAGCGAG ACCCCGCTTT  
21851 TCAAAAAATT AAAAAATGAG CAGGGAATTG GTGGCATGTG CCTGTGGTCC  
21901 CCAGCTACTC TGGAGGCTGA GGTGTGGGAG GATTGCTTGA GCCCAAGAGT  
21951 TGAAGGTTGC AGTGAGCCAT GATTGTGCCA CTGCACTCCA ACGTGGGTGA  
22001 CAGAGCAAGA CACCTACTGA AAGAAAATAA AGTTGAAGTT AAAACTTCTG  
22051 GCCAAGAACC AGCACTGGTT ATGATAGTAA CTCATTTTCT GTTGTGCAGA  
22101 TTTATTTCAAG AAACCTAATT TTAGGTTGTT GAATAGAAGT TTTGATCAGA  
22151 TAAAAATTGAA TTAACAAAAA TTTTTTTTGA GACAGGGTCT TGCTGTTATC  
22201 CAGGCTGGTG TGTAAGTGGT TGATCACGGC TCCCCGCAGC CTCAACCTCC  
22251 TGGGCTCAGG TGATCCTCCC ACCTCAGCCT ACCGAGTAGC TGTAACCTACA  
22301 GTGCATGACA CCATACCAGG CTCATTTTGT TACATTTTGT GTAGAGAGAG  
22351 GGTTTTGCCA TGTTGCCAG GCTAGTCTCA AACTCCTGGC ATCAAACAGT  
22401 CCTCCCCTC TGGCCTCTCA AATGTTGGGA TTACAGGCAT GACCAGCCAA  
22451 TTATTTCAAG GAGTTAATTT TTTTCTTCTA CTTTGGGGGA AGATGAATTA  
22501 TATAAGTCTC CATTTTAGGA GTATTTCTAC CAAAAGAACT ATTATCTTCA  
22551 AATATATTTT TGGATAGTAC TATAGATATA CTAATTTTGT TTTAAATTTC  
22601 TAGTAATTTT TTTGAAGATT TTGTATAGCT GTCCAAAGCC AATTTCTGTC  
22651 TACCTAATTT CAGCAAGATT TCACTCTTTT CATGTTACTT TTGTCCCAGA  
22701 ACAAATTTCA AGTGCTTTCT CTTCACCTGT GCATTCCTCC CCCTGATTAG  
22751 TCTCTGGCTT TGTATTACTT TCAGTCAGAG ACGACTTTT TTTTTTGAGA  
22801 CAGGGTCTCA CTCTGTCAAC CAGACTGGAA TGCAAGTGCA CAGACAAGGC  
22851 AGCCTTGACC TTCTGGGCTC AAGCAATCTT CCTTGCCCTC AGCCTCCTGA  
22901 GTAAGTGGGA CCACAGGCAC GTTGCCACCA TGCCTGGCTA ATTTATTTTA  
22951 ATTTTTATTA TTTTGTAGAC AGGGTATTGC TCTGTCACCC AGGCTGGAGT  
23001 GTAGTGGCAT GATCAAGGCT CACTGCAGCC TTCACCTCCT GTGCTCAAGC  
23051 AGTCCTCTCA CCTCAGCCTC CCCATTAGCT GGGACTATAG GTCCACACCA  
23101 CTACACCAGG CTAATTTTGT TAATTTTGTG GTAGAGACAG GGTTTCATCG  
23151 TGTTGCCTAG GCTGGTCTTG AGCTCCTGGG CTCAAGCGAT TCACCTGCCT  
23201 TAGCCTCCCA GGTGTGAGCC ACTACACTCA GCCTTTTAAA ATTTTGTACA  
23251 GAGATGAGGT CTTGCTTTGT TGGCCAGGCT GGTCTAAAAC TCTTGGGCTC  
23301 AAGCAGTCCC CTCTCCACAG CCTCCCAAAA TTCCGGGATT ACAGGCGTGA  
23351 ACTTCGGTCA TTTCTTAAC TTTACCCTTC CTAATGACAC TCCAGAGCTT  
23401 ACCTTCTTTA CTTTGTCTTC TTAAGTTAAC TAATAGACAA TTATTGTATG  
23451 TGGATATTGC ATTAAGTTGT CTTAGGATAC CTTTTTCAGA GGAGGACAGC  
23501 TTTTGACAAA TTGCTGTCGC GGAAAAAAA AGTATTGTCG AATTAAGAGT  
23551 TGCATTTACT GAAATCTCTG TTGAGAGAGG GGAAGTTACG TTGTCTCTAA  
23601 AAGAAAAACT AAAAAAGAAA GGGGAAGTTT TAGCAAAGTT GTTAAAGCCT  
23651 GACACTTAAG TCATACTACC TAGTTTTGAA CTCTTAGCCC CTGCCACAGA  
23701 CACGGCAGCC CCTTGAACCT TCCTGGGTTT AAGCGAGCCT CCTACTTCAG  
23751 CCCCCTGAGT AACTGGGACC ACTGGCCTGT GTCAGTGTG CTGGCTAATT  
23801 TTTTTTTTTT CCTCACATGG GCAATGTTGG GCAAGTTAAA TCGACTTCTT  
23851 TGTGCCTCAG TTTCTCATC TGAAATGGAG ATCATACTGC TATGTACCTG  
23901 ATACAATGTT TGTGAGGATT GAATGTGCAG AGTTCTTTT TTCTGTTGTT  
23951 GTTGTTTTGA GACGGAGTCT CACTCTGNNN NNNNNNNNNN NNNNNNNNNN  
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TCTCGTGATC  
24101 CGCCCGTCTC AGCTTCCCAA AGTGCTGGGA TTACAGGCAT GAGCCATCGT  
24151 GCCCGGCTGA ATGTGCAGAG TTCTTAAAAC CGTGTCAAGA ACATAAAATA  
24201 GTTATTTGTT CTTTCATATA ATGATGATTT TGAGGGCCTG CGGATCTTGA  
24251 CATGTTATCA GATTGGTCAA AAAAAGATTA AACCATAGTT GGTATTGTCC  
24301 TAGTTCCTGT TACCAGAATA TTCCATCTTT CATCGTTGCC TTCTCTCATA  
24351 GTTTTATGTA TCAAAAAGTT TATTGTAAAG CTAGGCCGGG CACGGTGTCT  
24401 TGGGCTGGTA ATCCAGCAC TTTGGGAGGC CAAGGCTGGC AGATCAGTTG  
24451 AGGTCAAGGAG TTCGAGACCA GCGTGGCCAA CATGGTGAAA CCCCCTCTCT  
24501 ACTAAAAATA AAAAATTAGC TGGATGTGGT GGTGGGTGCT TTAATTCCAG  
24551 CTAAGTCAAG AGCTGAGGCA GGAGAATCAC TTGAACCCAA GAGGCAGAGG  
24601 TTGCAGTGAG TTGAGATTGT GCCACTGCAC TCCAGCCAG GGGACAAAGT  
24651 GAGACTTGAT CTCAAAAAA AAAAAAAA AAAGTTATTG TAAAGCTAGA  
24701 CACGGTGGTA TTTGCCTACA ATCCAGCTG TTCGGGAAGC TGAGGCAGAA  
24751 AGATTGCTTG GGTCCAGTAG TTTGAGTCTA ACGTGGGCAA ATATATGAGA

FIGURE 3H



24801 CTCCATCTCA AAAAAAAAAA TAAAAAATAA AAATAAAAAA ATGTTTACTA  
24851 GTTTTTTTCA GTAGCCTTTT ATTATAGTAG CAGTACATGT GTATTGTAGA  
24901 AATTTGGAAA ATACAAGTGA AAAATAAAAA CATCAAATTC CCGTCAGCCA  
24951 GAGACTGCTG TGAAATGTTT TGAGCACATC CTTCTTGAAT GTTTTTTAAA  
25001 TCCTGGTATG TATATTTGTA TTTTAAAAATC AAAATGCATT CTTACCCATT  
25051 CTCTTTTGAA CCTGCTTTT TGTAGCTAAT GATCTCTAGT GTGTCCATTT  
25101 CAGTAAAAAT TCCATTATTA AAGTGCCTTA AAAATCGTCT CTTACAGTAC  
25151 TGCCACTATG TTGCTGGGCT GGTCCGAATT GGCCTTTCCC GTCTTTTCTC  
25201 AGCCTCAGAG TTTGAAGACC CCTTAGTTGG TGAAGATACA GAACGTGCCA  
25251 ACTCTATGGG CCTGTTTCTG CAGAAAACAA ACATCATCCG TGACTATCTG  
25301 GAAGACCAGC AAGGAGGAAG AGAGTTCTGG CCTCAAGAGG TAACAGATTC  
25351 AGGGTATTTT GGGGGAAAAT AACTTTAGAC ATTCTCTGAA AAATCCTTTA  
25401 ACTCTTGTGG TTGCGGGTGA CAGAAAAACA AGCCAGGCCT CCCCCAGGCA  
25451 GCATAAGGGG ATGTGGAAAA TAGGATAGAT TGACATGAGT TTGCTTCAGG  
25501 TAGACTGGCT GACTCCAGG ATTCACACCA CGTAATCAGT ATATTCAAGC  
25551 CTTGCTGTCC TTGATTTCTT TCAGACGGTC TTTCTCCAAG TGGTGGATAT  
25601 GGTAACAACC CACGTGCACT AGCTTAACAA AAAGTTCTTA GGAATGGCTT  
25651 TGTTCCGGCT GCGCAGTGG CTCATGCCTG TAATCCCAAC AGTTTGAGAG  
25701 GCCAAGGTGG GCGGATCACC TGAGGCCAGG AGTTCGAGAC CAGCCTGGCC  
25751 AACATAGTGA AACCCTGTGT TTACTAAAAA ATACAAAAAT TAGCCGGGCG  
25801 TGGTGGCAAG GGCTTGTAAAT CCCAGCTACC TGGGAGGCTG AGGCAGGAGA  
25851 ATCGCTTGAA CCGAGGAAGC AGAGATTGCC GTGAGCTCAG ATTGTGCCAC  
25901 TGCACTCCAG CCTGGGCGAC AGAGTGAGAC TCCCTCTCAA AAGAAGAGGA  
25951 AGGGCTTGGT TCTTCTGCTC AGCCCTGAAT CAGTTACTGT TGCTACACAG  
26001 CTGAGTTCTC TGGCCTCACC TGGATTACGT CTACACAGTA CACACAGAAT  
26051 GGATTTCCCC CAAAGAAAGA ATTCTGCGGC AGGAAGGGGA AAGGGATGGC  
26101 AGGTAGACAA AAATCCAGG TGTCTGTAAT AAGGGACAGG GTCGATCTTT  
26151 AATTAAAAACA TGGACAGGGA ACAGAAAGCT TTTGATACTG ATTTTGTTC  
26201 GAAGGAAAGT AGAAAAATTT ATGACTGTCT CCTGAATTTA TTCCAGCATT  
26251 TACCTTTTGC TTTCCATAAA AGTGTTCCT GCAGCCAAGT ACTTTAAAGT  
26301 TTTAAAAAGA CGGGTGAGGC TAAGTGTGGT GTCTCATACT TATAATCCCA  
26351 GTGCTGAGGC CAGGAGTTCA AGACCAGCCT GAGCAACACA GCAAGATACC  
26401 ATCTCTATAA AAAATTGTTA GAAAATGATT CTGCTGAAAG AGCAAAAATA  
26451 AAAATTAAAG AAAGTAGAAA AAATAAAACT AAATTTAAAA GATTAAGTGG  
26501 GCATGTTGGC ATGCACCTGT ATTCCTAGGT ATTCGGGAGG CTAAGGCACA  
26551 AGGATCCCTT GAGCGCAGGA GCTCAAGGTT GGATTGAGTT GTAATCACAC  
26601 CACTGCACTC CAGCCTCGGT GGCACAATGA AACTGTCTCA AGAAAAAATA  
26651 AAAGTGACAG AGGGAAACAA TATTTGCAAT TCATAGAGCA GATACAGGGT  
26701 TCATATTCCT AATATTAAAA AAAACTTCTA AAAGTTAAGA AAAAGGCCAA  
26751 CTGCCCCACA GAAAAATGGG CAAGGAGATA AGAACAAGAT TGTTACACAGG  
26801 AAGAGACACA CAGATGATTA TTAATAATCT GAAAAGATGC TGAGTCTTAC  
26851 TCCTAAGAAA AATTCACATT TAAACTACTC TGGGGGCTGG GCAAGGTGGC  
26901 TCACGCCCTG AATCTCAACA CTGGGAGACC AAGGCAGGAA GATCACTGAA  
26951 GCCAGGGTAT CGAGACCAGC CTGGACAACG TAGTGAGACC TTATCTCTTA  
27001 AAACAAAACA AAACAAAACA AAACAAAAAA AACAGTAAAA ATTGGCCGGG  
27051 CACAGTGAAT CCTGCCTATA ATCCCAGCAC TTTGGGAAGC CCAGGTGAGT  
27101 GGATCACTTG AGGTCAGGTG TTTGAGAACA GCCTGGCCAA CATGGCAAAA  
27151 TTCCGTCTCT ACTAAAAATTA CAAAAATTG CCAAGTGTGG TGGCATACGC  
27201 TGGTAGGGCC AGCTACTTGG GAGGCTGATG TGAGACTCCA TTTAAAAATA  
27251 AAAAATCAAA AATTAGCTGG GTATAGTGGC ACACCCCTAT AGTTCTCGCT  
27301 CTTGGGAGG TTGAGGCAGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT  
27351 GCAGTGAACC ATGATCACAC CACTGCATTC TAGCAGCTG GGAGACAGAG  
27401 CAAAACCTT GTCTCAAAAC AAACAAACAA CAACAAAAAC AAAAAACACT  
27451 TCCCTCAGCT CAGACATGGC CTTTAAAGTT TCCTAGGTGA CTCGTGTGCA  
27501 GCCAGGGTGT AGAAACCACT CTTGTCTTAC CCCTCTTTG CAGACACAGG  
27551 GCTCAGAGAA GGAAGGGGA TTGTCTGGGG ATGTATAGTG AGGCAGTGGC  
27601 TGCCTTGGA GTGGAGTCTC AGTCTCCCG CTCCTAGGCC AGCCCCTGAC  
27651 CACTGTTCCA TTGTCTCCA GACAGAACAT CAGCCACGGG CATGTGATGC  
27701 ATGAGCGTGA GCCACACCAT CTTGCACACA CAGGAGCAGA GCCCTGCTCT  
27751 TCTCATTCAC TTACTTTATC TGTAATAATAG CATCATTTCT ACCACACGGT  
27801 GGTGGTGTGA ATAAATGAG ATGAACCTCT AGCATAGAGT GCTTAGTAAA  
27851 GGTTCCTGGAC ATTTCTAGT AGTTGAATCA TGCCAAATGT GGTCTAGGT

FIGURE 31



27901 GATTGGCTTC TTTTGCTAGC ATGTTTTTCAG GGCTCCTCCA TGCTGGGGCA  
27951 TTGCATCACT GCTTTATTCC TTTTATATCGC CTAGTATTAT TCCACTGTGT  
28001 GGATAGACCA CATTATATCCA TTCATCAGTT GGAGGATATT TGGGTTCTTC  
28051 CCATTTTTTTT TGGCTATGGT GAATAGTACT GTGTACATTT GCATATAAGG  
28101 TTTTGTGTAG ATGTGTGTTT TCCTTTTTTCT TGGGTCTATG CTGAGAAGTG  
28151 GAATTGCTGG TTCATACAGC AGCTCGAACC TTGTGAGGAG CTGCCAGACG  
28201 CTTTTCCAAG GTCGCTCCAC CATTTTACAT TCCCGTCAGC AGTGTGAGAG  
28251 TCCCAGTTTC ACCAGCACTT GTTGTTATCT CTTTTTAACT GTATGTATAT  
28301 ATACTTAACA TTTTATTTAT AATAAATGTA CATAATAGAG AATTTGCCAT  
28351 TTAACTATT TTTAAGTCTA TTATTCAGTG GCATTAAGTA CATTAAATGAT  
28401 GTTATATAAC CATCAACACT ATGTTTCCAG AACTTTTCGCT AGCTTCAGAG  
28451 AATCCTCTAA ATAATATCAT TAAAAATCAT CAAGCCGAAT CCCACTGTTA  
28501 GAATTAAAGG TTTTATTTCA CTTTCAAGTT ATCAGGATCC AGGGAGGTGT  
28551 AATACACTTA GAGGATAGAC TCAGCTCATT TCCCAGCTAT GCCTTTCAGC  
28601 AGCATCTTTA CCAGAGTAGG AATATAATGT TAGTCATTAT TTAGAGGCCT  
28651 GGCCATCTTG AGAAGGTTTA CTGTTTAGTC TGCAGTACAA TTATAACTGT  
28701 TTTTGTATAT TGGGTTATTT TTTTCAGAAG TAGGCCAGTA GCTCTAACAG  
28751 GAGCCTCTTT AGCCTGAATT CGTCCAAGTA GTGCAGTGT GCAC TAGTTG  
28801 TCCCTCGGGA CATGCTCCCC AATACGTAAC TCACTTCCAG GTTGCAACTG  
28851 GACACTTACT GGTAGTCAGA AATAGCTATT GCATGGAGCT TAAAATGAAC  
28901 TTGATCTTCG TGAAAGATGA GTCTGCAGCT AAGAGACTTT ACTGTATATC  
28951 ATAGTGTTTT TTTTGTTTTT GTTTTGTGTT TGTTTTTGTG ACGGAGTCTC  
29001 ACTCTTTCAC CCAGGCTGGA GTGCAATGGC GAGATCTTGA CTCACTGCAA  
29051 CCTCCGCCCC CTAGGTTCAA GCAATTCTTC TGTCTCAGG TCCTGAGTAG  
29101 CTGGGATTAC AGGCGCCTGC CACCGTACCC GGCTAGTTTT TGTATTTTAA  
29151 GTAGACACAG GGTTCACCA CCTTGGCCAG GCTGGTCTTG AACTCCTGAC  
29201 CTCGTGATCC ACCCTCCTCG GCCTCCCAA GTGCTGGGAT TACAGGCGTG  
29251 AGCCACGGCG CCCAGCCTGT ATCATAGTTC TTATGCACAA AGACCCTTTA  
29301 ATATTGTTTT TAAATTCTCC CCTATGCACA CGCTGACCTG TTCCTTAATC  
29351 TTCTTATCTG TCTAGGTTTG GAGCAGGTAT GTTAAGAAGT TAGGGGATTT  
29401 TGCTAAGCCG GAGAATATTG ACTTGGCCGT GCAGTGCCTG AATGAACTTA  
29451 TAACCAATGC ACTGCACCAC ATCCCAGATG TCATCACCTA CCTTTCGAGA  
29501 CTCAGAAACC AGAGTGTGTT TAACCTCTGT GCTATTCCAC AGGTAGGGAA  
29551 CGGGGCTCCT CTGGGTGGAT ACGGGGCTAA AGGGAGTGGG GTAGGAGTAA  
29601 GGGTGGATT TGTGTGCTA TATTCAAGGA TATGATTCCT TAAAAAGACG  
29651 ATGACTCCAG TTTATTACGC TGGGAGTTTC ATAGCACCCG CCTTTGCTTC  
29701 CAGCCACCAA ACTCAGCTCA GCCTTGAGGT TAAGCCTGCT CCTTTTCAGA  
29751 ACCTTCTTTC CGGATTTACT ATTTTCTACA GCTATCCTAA ACTAGTTAGG  
29801 TTCTTTTCTC CACAGTTAAG TCAAGGTCTT TGGCTTAGAT TTATGGGAG  
29851 TGCTGGGTAA AACCTGGGTG AAGCTGTTAT CATTAAAAAG TCTTCATTAA  
29901 GCACCTAATT ACTGCTGTCC TTTTCCTAGA CCCGGCATAA AAAGAACCTG  
29951 GTCCGGTAGA CCTAGCCTCT CAGTATGCTA GGAACCTACA CTTTTTAGTT  
30001 GCCTTTACCA AGTATTGCAG ATACTACTGC AAATAAGTGA AGAAAGTAAC  
30051 AGCATTTAAC TGATTTGGGA ACTTGGTTTG ATCTTGTCTT AATGACCCAC  
30101 TTCGAATGGT GGTTGAAAGT AAAATCTGTA TCGCCGTCTT ATGTTTCCAT  
30151 TTACCTAGAA ATACTTTACC TTTGAGCACA GGAAATTAAT CCCCTTCTGG  
30201 TTGTTCTCCC CCTGGCATTG GTTTTAAATA TATAATGATT ATGTTTGTG  
30251 TAGGAAAAAT AGAAAAACAA CTACAATAGA AAATTCTTCC CATATATTAT  
30301 TTTGAAATAC ATATTTCCGA TCCGATAATC CATTGCTCTA GCATGGAAAA  
30351 TGTTGGATT ACTTGTGTTT GCTTTTTCCA AATAAAATGG AACTTTTGTG  
30401 GCTACATTAT AGAATTGTTT TAGACTGCTT AATTCTGTGT GTTGTGAGA  
30451 AAGGGAGGAG TGGGGAAGGT AAAAATCTTG ACATACTTTC TTCGTGGGTA  
30501 TTTTTTCTTG AGCGATTCCA TCTTAGTTGA TTAGCAGTTA GCAATTGCCC  
30551 ATTCAACAGA AGGTTTTCTT ACCTTTTTGT GATAATGATA GCTAACGACA  
30601 TCATTTCTTC TTTTTTCCCT CTCTTCTTGT TGTCTCTAGG TGATGGCCAT  
30651 TGCCACTTTG GCTGCCTGTT ATAATAACCA GCAGGTGTTT AAAGGGGCAG  
30701 TGAAGATTCG GAAAGGGCAA GCAGTGACCC TGATGATGGA TGCCACCAAT  
30751 ATGCCAGCTG TCAAAGCCAT CATATATCAG TATATGGAAG AGGTGGGTTT  
30801 TTATTTAACT ACTTGATAA TTTGTAGCTA CTTTTATGAT TTAGTAATGT  
30851 CACTGTTTAA CCAGGTTTGG ATATTAGATG ATCCTAACAA TTCACTATCC  
30901 TGTGGCCTAA AGAGACGGA ATTGATATCC TTTATAAGGA AAAAAGTCTA  
30951 TTCACAGGAG CCGAGCAGAT TGCTCACTGC TGTGTAGTAC CCTGGTGAGA

FIGURE 3J

31001 GGAGATAAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCTCAG TAGAATCATA  
31051 GATTTTGGAGC TGCAAGATGA TGCAGGAGGC CAACCAAGCT TCTTGTGCT  
31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT  
31151 GAGTGGATCT CTGGCTCCCG TCCATGTGTC CTGACACCCA GTCTGGTACT  
31201 TTCATTATGC CACAGGCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC  
31251 CAAGGAAAGC CATCAAGTTG CAATTATTTC CTAAATTTC TTTGGAAAAAT  
31301 TTCATTTCAA ATACCAAAAC CATCCTATAA AAAGAAAACT TACCTTCTTA  
31351 GGTCAAATCT CTAATATTG ACTAGGTTCA AAAAGTTTAT TTCTGGCCAG  
31401 GCACAGTAGC TTACTCCTGA AATCCCAGCA CTTTGGGAGA CCAAGGTGGG  
31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG  
31501 ACCCCATTTC TACAAAAAAT TTA AAAAATG TCATGGTGGT GCACGCCTGT  
31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGGATCACAT GAGCCTGAGA  
31601 GGTCGAGGCT ACAGTAAGCT GTGTGATTTC ATCATTGCAC TCTAGCCTGG  
31651 GTGATAGAGT GAGACTTTGT CTCAAAAAA AAAAAAAAAA AAAAAGTCTT  
31701 AGAGACAGA AGTCTCTGA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG  
31751 TGGTTTGTAA ATGGAGGTGA TTTGCTCCCC TCCCCCAGA GGACATTGGA  
31801 CAATGTCTGG AGACATTTTT GATTGTCTTA ACCGGCAGGA ATCGGGTGCT  
31851 ACTGGCATCT GGTGAGTAGA GGCCAGGAT GATGCTGTGA TCCTCAGGTG  
31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAA CATACAAGAC  
31951 CCTCATCATT TTTCTTTGTC CTGAGCTCCC TCCCCAGAGG TTACCTCTGT  
32001 TCATGGTTTT GTGCATCCGT CTAGTCCCC TGTTACGCGT TTACAGGAAT  
32051 ATGTTTTGCA ACAGTGTTT CATCTAAATA GAATTATACA AAATAGCGAT  
32101 TTCTGATTTC TCTTGATAT TGCACATTCT TCTTATACTT CCTCCCTACC  
32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAATTCTAT CAGAGGCACC  
32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAAACC CTAAATTTT  
32251 GTAGTCACTA GATGAAAATA TTCAGCCAGT GACCCAAAAA ATTGCTACCA  
32301 ATGAGACTCT CCATTTTGCC ATGTAGCCAG AACTTACTTT GATCTATGTG  
32351 CCTGGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG  
32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA  
32451 CATCAGAATC CATGATGTTA ACCCAATTC TAAGGGGTTC AACTACCTT  
32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCAT TTTATATAAA  
32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTTTTG GTTTTGCACT  
32601 TTGATCACTA GTTTTAGAAA CCAGTTTTTA AACACTTTGT GGCCAATTCC  
32651 ATTACTATAT TAAATTCAG ATTTATTTGG TTTTCTCTTA ACTATTGGGA  
32701 TTAATCCTG GTTGTAAATC ATAGTTTGAG GGCGAGGGTG GGCAGTCTAC  
32751 ATTTGGCTGA GCCCTGTTT TGTGAATAAA TGTTATCAGA ACACAGCCAC  
32801 ACCCATTTGC TTCTATGTCT TCTGTGGCTG CTTTGTCAAT GTGACGCCG  
32851 AGTTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTTT  
32901 GGCCCTTGAA TAAGAGGTG GCTGACTTCT GACTTAGGGC ATCAGTTGTT  
32951 CTGTTATCCC AGTAAACTC AAGGCATTAG GGGAGAAATG TTAATATTAA  
33001 TACTTAAGTT GATTTGATT AGGGAAATCT TTGAAGATT CTAAGTCTTA  
33051 AGCAGTAGAA CCTGTTAATG GTTTTAGTT CAGCAGTAAG GACATTTAC  
33101 AAGTAAAGTT TTAATGAAA ACATTTTGTA TGAAGCCACA AGTCGTCTGG  
33151 CCTCTTGCTG GTGTCCAGAT ATTAACACTG ATCCTATTTC TCCTTGCTGA  
33201 CCAAGTCTGT CTTTTGTAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA  
33251 TCTCTGGACT TAGTGTGTGA GCGAGCATGC ACCTGGAAGG GACTTGCCAG  
33301 AGGACCTCCT CATGCTTCTC CAGTGCTTAG TGGGGGCTTG GAGTGACGCC  
33351 CCAGGTCCTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCACTCT  
33401 GGAGCAGCCT CTGCTTCAAA CCAGCCTGGA TGCTTGTGAG CTGGGGAGAA  
33451 GATCAACCTG CTATTTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG  
33501 AAACCCCAT TCCCCTCTCT GCCAAAGTGA ATTCCTTGGC AGGGAGAAGC  
33551 TTGTTCTGTT CTCTGCACAC TTCCTGTGCC CTCCTGTGGT TAAGTCAGAG  
33601 AATCATCCGG CTCTTTGAGC CCCAGGTGCC TAGCTGCTCA AGGATGGTCC  
33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCATTA GACATCCAGC  
33701 CCCCACCAA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CCAAATGATG  
33751 TTTTTGCTTT AATGGAAGTT TAGATGTTCA TAGACAAGAG TTTTAAATGA  
33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT  
33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT  
33901 GCACAAGAGC TTATTTCACT CTAGTAAACA TTTATAGGAG CCTGTGTCAT  
33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CAAAACCTTT  
34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC  
34051 TGGCCAATAT GGCAAAACCC TGTCTCTACT AAAAATACAA CATTTAGCCA

FIGURE 3K

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34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCGGAG CCTGAGACAT
34151 GAGCATCGCT TGAAC TCGGG AGGTGGAGGT TGTAGTGAGC TGAGATGGCA
34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTTT CTCAAACTCC
34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC
34301 TATGACCTGT CCTTGACAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG
34351 GTTTTTAAGA CCTGAATAAT TGAGTTTGCA GAAACCTACT GTGTGCCTTC
34401 AGGTAAATGG AGAGTGGGGT TTGGTCTAGC AACGAAGCAT CTAGAAGGTC
34451 TCTTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCAG
34501 TGACTGCAGC TCTTCCAGTT GTGCTGTCAT GTTTATATGT TAGAAATGAT
34551 CATCAAAGGA CTCAAAAGTT TTGCCACTAA TTGTATTACC GGGGACTGTC
34601 ACAACCAAGA TTTCTCTTAA TTTATTCACT TTACTTATCT CCTGGAAGGG
34651 CATATTGAAG TGCTCTTGGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT
34701 ATATTCACCT GGGTGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTC
34751 CCAAAGGAT GTAAGATGGC TTATGGTTAT AAGTACAACA GGCTAACAAA
34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAGTCA TAGGAGCCAC
34851 AGAATTAAAC CAGGAATGAA TAAGTGTGTA GTTTGGTGCT GATGTTATCA
34901 TCCTTTATTT GTACATTGCT TGTACAGTTG CTCTGAGAAG GTAAGTCTTA
34951 AATTTTCAAA AGTGAAATGT CACCGAGCAT GGTGGCTGAT GCCTCTAATC
35001 TCAGCACTTT GGGAGGCTGA GGCAGGCGGA TCACCTGAGG TCAGGAGTTC
35051 GAAACCAGCC TGACTTATGT GATGAAACCC TGTCTCTACT AAAAAAAAAA
35101 AAAAAAAAAA AAAAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG
35151 CAGGTGCCTG TAATCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA
35201 TGAACCTGGG AAGTGGAGGC TGCAGTGAGC CAAGATTGCA CCACTGCACT
35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAATAAAAA AAAAAAATCT
35301 ACAATATACC AAAACCATTA CTTACCTGAG AAATATTCT CAGGGTCATT
35351 GTAGTGAATG CCTATTTTAT GGCTTTTGAT GGCATCAGGG CACTCAGGTC
35401 ATTTACAAGA GTAGTGTGTG AGACCTGTG TGTCAC TGCC ACTCATCTTG
35451 GCCTTCGGCC ACTGCTGTAG CAACCAAGTT CCAAGTAGGG CTGGACCTTG
35501 CCTTCTGCTC CAGAGACCTC TCGCTTCTCG CCCTTGGGCT TCTGACGAGC
35551 TGCAGGAAGT GCCTGGCAGC TGGGTCCCCA CAACCCAGAG GAGGTGAGGG
35601 CCACCTCTCT GCTCCTCAGG GCCACCTTTC ATAAGGCTCC TTGAAGGTCC
35651 CTCAAGATCA AGCCAACTCA ACACATCCTT GATAGGCCTT CCTGCCTTCT
35701 GTTTCACCTC TCCACTCGTT TCCAAATAAA TGGCTGCATG CAAGCTTTTG
35751 CCTCAGGTTT TGCTTTTAGG AGGAAGGCTA AGACAAGCAG TAAAGCAACA
35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT
35851 TTTACTTTTAT GGATGCTTGT ATTGAAAAGT CTTGGCTGGG TGGAGTGGCT
35901 CACGCCTGTA ATCCCAGCCC TTTGGGAGGC CGAGGTGGGT GGATCACTTG
35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGCTCTC
36001 TATTAATAAT GCAAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC
36051 ACAGGGCTAG GCTGGAGATA AAAAGGTGAG TAAGTAGGTG CGGTGTAGTC
36101 AGGGTGAAAA CTACAGATGG TCCATTTCCA CGTAAGTGGA AAGGTAAAGG
36151 TATGTACAAT AGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT
36201 TCTAGAAGGC ATAATCCTGA AGTTGAGACT TGGGGGCTA GGTAGGAGCC
36251 AGTTGAAGGG ACGTGGGAGG CGCATTCAG AGAGAAGGAG TGGTATGAGA
36301 CTGGAACAGA GGTGTGCAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA
36351 GTTGTCTCTT TGTTTTTGTG TGTTTTTTGA GACAGGTCT TGTTCTGTCA
36401 TCCAGGCTGG AGTGCAGTGG CATGATCTCG GATCACTGCA ACCTCCACCT
36451 CCCAGGCTCA AGTGATCTTC CCACCCAGT CCCCAGTAG CTGGGGGACC
36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTTGTACATT TTGTAGAAAC
36551 AGGGTTTTTAC TGTGTTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA
36601 GTCTACATGC CTCAGCCTCC TGAAGTGCTG GGATTCCAAA CATGAGCCAC
36651 TGTGCCTGGC CCGGCAACTG TTAGTAGACT ATAGAGAGGG AGGTGGGCAA
36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT
36751 GCGCTACACA TTACAGAGCT CAGGCTTTTT TTCTCCAGGT GAGAGGGCTG
36801 GTGCCACTGA GGCATCAAGC AGAGGTTTGA GATCTCCTTG GTGACAGTGT
36851 AGAGCAGACA GGTAGATTG GGAATTTAAG CTTAGACTCA CGTTGGAGAC
36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT
36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTTGT
37001 GGAGGAGTGG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG
37051 CTCCCTGCTT CTGTTCTCTG CCCCCTTTGT CAAGCTGTGG TCTGTACTGC
37101 GTGTTCCATC TTGTTTCTAA GCTGCTTTTG CCCAGTCTTT CCAGCATTTT
37151 CCTTTCGTCA TGTTAGTCTG TGCCTGTCTA CGTGAACAT GGTGACGTTT

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FIGURE 3L

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

```
37201 ATTGGGCCTG GCACTGTGAG GTGCTGGGGA TGTGAAGATC ATTGTGGCTC
37251 AGCCGCTGCT CTCGAGGGCC TCTGGGTGCA GTATGCACAC CTGTGCCTCC
37301 TGTTTGCTCA GGAAGACAGG CTTTGAGATG AGCTGGGGCT GACATCCCCA
37351 CCTTATCATT GGGATGGCTT TGGGTAAGTT ATGTTTCATGT TCTCTGAGCC
37401 TCCCTTTCCT CATTGGTAAA ATGGGTATAA AATACCTGCC AGTGGAGGGT
37451 TGTTGTAAAGT AGCCATGGAA AATGTAAAGC ACATAGCACT TACCATTTTT
37501 TCCTGTGTCT TTAACAGATT TATCATAGAA TCCCCGACTC AGACCCATCT
37551 TCTAGCAAAA CAAGGCAGAT CATCTCCACC ATCCGGACGC AGAATCTTCC
37601 CAACTGTGAT CTGATTTCCT GAAGCCACTA CTCCCCCATC TACCTGTCTG
37651 TTGTCATGCT TTTGGCTGCC CTGAGCTGGC AGTACCTGAC CACTCTCTCC
37701 CAGGTAACAG AAGACTATGT TCAGACTGGA GAACACTGAT CCCAAATTG
37751 TCCATAGCTG AAGTCCACCA TAAAGTGGAT TTACTTTTTT TCTTTAAGGA
37801 TGGATGTTGT GTTCTCTTTA TTTTTTTCCT ACTACTTTAA TCCCTAAAAG
37851 AACGCTGTGT GGCTGGGACC TTAGGAAAG TGAAATGCAG GTGAGAAGAA
37901 CCTAAACATG AAAGGAAAGG GTGCCTCATC CCAGCAACCT GTCCTTGTGG
37951 GTGATGATCA CTGTGCTGCT TGTGGCTCAT GGCAGAGCAT TCAGTGCCAC
38001 GGTTTAGGTG AAGTCGCTGC ATATGTGACT GTCATGAGAT CCTACTTAGT
38051 ATGATCCTGG CTAGAATGAT AATTAAAAGT ATTTAATTG AAGCACCATT
38101 TGAATGTTCT TACTAGTAGA AAATGATGTG AATTTTCTTT CTGTTGGCT
38151 CCTATTTTTC TCATCATTTT GTTTTCTTTA ATTGGGTTGA ATGGAGTAGA
38201 TAGAAATATT TATGGTTTAG GTAACAGTTA GATGTTTCCT AAGAATGCAA
38251 ACTGCCCTTT CCACACAAG GCTGGGAATA AAATTCTGGG TATTCTCGTA
38301 TTCTCATTTA AAGGAGTTTA GCTTTCAGAG AGAAACAGCA GGATTGCTTT
38351 TGACCTTTTA GAAGATTGGT CTCCAGTAAA GGTGGACATT TTTGAGATTT
38401 TTATAATAAA GAATTTAATT GCTCTGCATT TGTCAAGTAC AGTTCGCTTG
38451 AAAGCCTGCC TGACTGTGGA AAAGATGGAG CTCAAGAATG GAGTTGATGG
38501 CCCAGCGTGG TGGCTCATGC CTGTAATCCC AGCACTTTGG GAGGCTGAGG
38551 CGGTCGGATC ACGACATTAG GGGATCGAGA CCATCCTGGC TAACACGGTG
38601 AAACCCCGCT CTCTACTAAA AAAAAAAAAA ATTAGCCAGG CGTGGTGGCG
38651 GGTGCCTGTA GTTCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCTTA
38701 AACC CGGAG GCGGAGCTTG CAGTGAGCTC AGATCGCGCC ACTGCACTAC
38751 CAGTCTGGGC AACAGAGCGA GACTCCATCT CAAAAAAGG AAAAAATTGT
38801 AAAAAAAAAA AAAAAAAAAA NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN (SEQ ID NO:3)
```

FEATURES:  
Start: 2058

FIGURE 3M

Exon: 2058-2156  
Intron: 2157-7996  
Exon: 7997-8094  
Intron: 8095-8869  
Exon: 8870-9053  
Intron: 9054-25147  
Exon: 25148-25339  
Intron: 25340-29365  
Exon: 29366-29542  
Intron: 29543-30639  
Exon: 30640-30792  
Intron: 30793-37517  
Exon: 37518-37736  
Stop: 37737

**CHROMOSOME MAP POSITION:**

Chromosome # 8

**ALLELIC VARIANTS (SNPs):**

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
825	G	A	Beyond ORF (5')			
2632	C	T	Intron			
4430	C	T	Intron			
4791	C	T	Intron			
4886	G	C	Intron			
4887	A	T	Intron			
4889	T	A	Intron			
5110	G	T	Intron			
6911	G	A	Intron			
7212	A	G	Intron			
7355	C	T	Intron			
7398	T	C	Intron			
7653	T	C	Intron			
8310	A	G	Intron			
8145	C	T	Intron			
8031	G	A	Exon	45	R	K
8462	G	C	Intron			
8873	C	T	Exon	67	N	N
9190	C	T	Intron			
9311	T	-	Intron			
9847	T	C	Intron			
10460	C	T	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	A	Intron			
21477	G	A	Intron			
22230	C	T	Intron			
22941	A	G	Intron			
23963	C	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	C	G	Intron			
27151	C	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron			
29572	C	T	Intron			
29761	C	T	Intron			
30732	G	C	Exon	281	L	L

**FIGURE 3N**

30841	G	T	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C	Intron
34532	T	C	Intron
36541	T	C	Intron
36607	A	G	Intron
36681	A	G	Intron
37493	C	T	Intron
37966	C	A	Beyond ORF (3')
37973	T	C	Beyond ORF (3')
38113	C	A	Beyond ORF (3')
38298	G	C	Beyond ORF (3')

Context:

DNA

Position

825 CCAGTGAACGTACCTGACAGGTTTCCTGTTTGTGTTTGTAGATGAAGTCTCGCTCTTGTTCC  
CCCAGGCTGGAGTGAATAGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCTGTGTTCA  
AGCGATTCTCCTGCCTCAGCCTCCCAGGTAGCTGGGATTATAGGCGCCTGCCACCATGCC  
TGGCTAATTTTTGTATTTTAGTAGAGACGCAGTTTCAGCATGTTGGCCAGGCTGGTCTT  
GAACTCCAGACCTCAGGTGATCCGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGC  
[G, A]  
TGAGCCACCGCGCTCGGCTAGACCTGACAGGTTTTAAAGGATTACTGGTTGCTGTGTTA  
AAACAGACTGCAGGATGGCTTAGGTAGCCAGTAGGTTTTTTTTTTTTTTGGAGACGTAGT  
CTTGCTCTGTTGGCTGGCTGGAGTGCAGCGGTGTCATCTTGGCTCACTGCAAACCTCCGC  
TTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCGGAGTAGTTGGGACTACAGGCGCC  
CACCACCACACTCGGCTTTTTGTATTTTAGTAGAGACGGGTTTACCATTGTTGGCCAG

2632 GCCGTCCTGGCTGACCTGTCCCTGCCCCGCAAGCCGCCCTGGGCATGAGCGACTTTTGC  
GTGGTTCCCGGTGGTTGCGCTCCCGTTTCGTCCCTCCGTGAGCATCGGCGCTTACCGG  
TATTTTAACCCGAGGGTTACACATCTGAGGCAATGTGGGTGGGTTACGCGGGAGAGGACG  
AGTGAGTTTTTTGTAAGCGGAATGAACTATGCAGATAACATCACATGAAGGCCGTTTCT  
GGAATGAAGTCTGACTCCTCCAGTTTACCACCTCTCCGGAGCTCTCCCGCCTTGCTG  
[C, T]  
CTTCCATCGCTTCATCCTCGGTGCTTCTGAGTTTTAAAATCGCCTATCTACGCTTCCAA  
GTTCCAATGAGTTATCTAACGTCTATGGATTAGCTAGGTGGTGGTGAAGGTCAGAAT  
TGGTTTTACTTAGATTTTATCTGCCTCATGCCGTACTATTGTTAATGAATGCATAG  
GAGGTGTTTTTATTTCCAACAAGAAAATTATTTCGTACGCGATTATTGAATGAATAGACAAA  
TTCAGCCAAGTTCTTCTGGTCTGGACCAGCCTGGCTGATTTCTGTAACTTTTTGGGCCA

4430 GGCCTTTTTTTTTTTTTTTTTTGTAGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT  
GTGGCCTGAACATGACTCACTCCAGTTTGACTTCCTTGGCTGAAGCCATCCTCCCACCT  
CGGCTTCTGATCCCGAGTAGCTGGGACTCCAGGCACGTGTACCAATGCATGGCTAATT  
TTTAAATTTTTTTGTAGACACAATGTCTCGCTGCATTGCCAGGCTGGTCTTGAACCTCT  
GAGCTCAAGCGATTTTCCACCTCAGCCTTCAAAGTGCTGGGATTACAGGTGTGAGCCAC  
[C, T]  
GCACCCAACAGTTTCTCTCTGCAAACTAGGGAAAAAATTTACGCTTAGCAGATATTGAG  
GGCTGATTATTTCTATCACAGAAGCATTTGGCTATAGAATTTACAGGTTTAGTAAACTTG  
ATTTACACTGAATTTTGGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT  
TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA  
GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT

4791 GGCTGATTATTTCTATCACAGAAGCATTTGGCTATAGAATTTACAGGTTTAGTAAACTTG  
ATTTACACTGAATTTTGGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT  
TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA  
GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT  
AAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAACCTTGGTAACTTAACCTCTGAAC

FIGURE 30

[C, T]  
ACAGTTACTTCATCTGTAAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAAC  
TCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCAGTTGGC  
AGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTT  
GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTAT  
TGCTATTTTTCTAAACACTAAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTT

4886 CTACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA  
AGAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTT  
AGACTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC  
AACCTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGT  
ATGTTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTT  
[G, C]  
AGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCAT  
CCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACT  
GACTAGGGTTGTATATGCATTTTATGCTTATTTCTAAACACTAAAAATGCTAAATTC  
TGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT  
TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4887 TACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA  
GAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTA  
GACTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA  
ACCTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGTA  
TGTTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTG  
[A, T]  
GTGTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATC  
CCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTG  
ACTAGGGTTGTATATGCATTTTATTGCTTATTTCTAAACACTAAAAATGCTAAATTC  
GCCCGAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGTT  
GATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGA

4889 CGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA  
GCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGA  
CTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAAC  
CTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGTATG  
GTAAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAG  
[T, A]  
GTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCC  
ACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTGAC  
TAGGGTTGTATATGCATTTTATTGCTTATTTCTAAACACTAAAAATGCTAAATTCCTGC  
CCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGTTGA  
TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA

5110 AAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGT  
CTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAA  
GTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATG  
AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTATTGCTTATTTCTAAACA  
CTAAAAATGCTAAATCTGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCT  
[G, T]  
TGAGACCTTAAAGGGTTGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA  
TGGAGTTAAGTGCTTGATAAATGGTGGTTATCAATCTGATTATGTAAATTTATGTAAATT  
CAGTTCTCAAGTTTGTGGTTTTTTTCCCCTCCTGGAGAAATCTATTCTATTTTAAAGTGA  
GGAAGGCTCCGTGGAGGGCTGGTAGCTGGTAGCTGTTCACTTGTGGAACCTTTCAGCCTGA  
GGCTGGAGCCCCCTCCTGGGAGTCTGGTCTTGTGCTTCTTGACCACCCACACCCCTT

6911 CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCGTGCGCCACTGCACCCGGCCCTGTT  
GGATAAATGATTCCAGTCTCTCCCAAAAAGAACTGTTGTAAGACTGTGGGGTGAGGGGAG  
GGAAGGGACAAATAGGAACCCGCCGTATTTTCCACTCCCTGTGGGCCTAAACTGCTCTA  
AAAAATAGTCCATGAAAAAATACATAGTACAAACAGCAACTCTTCTGATATGCTTGCAT  
TTAAATCAGGCTTTTTCTCCCTTTTGGAAAAACACAGTCCTTGTTTGCTTTAGGGAAGA  
[G, A]  
TAAAGGTCAGTGCGCTGCATTGCATTAATTTTGAAGGAAAGATGAGAAGACATCTTGAA

FIGURE 3P

AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGC

7212 TAAAGGTCAGTGCCTGTCATTGCATTAATTTTGAAGGAAAGATGAGAAGACATCTTGAA  
AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGC  
[A, G]  
TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGG  
AACCTAATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAA  
TTTAGCAGGATTCTTGGTAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTC  
CAGGCTTTATTGGGAAGAGGATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACT  
CTGTCACTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTTTAGCGGCCAGT

7355 CAAAACAGATTTTATTAGAAAACTACTGCAGTAAGAGGAGAGACCTCGGTACAGAA  
CTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGGGGAGCCGGATGTCAGT  
GGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTTGCTGAAGGCAGGCCAGA  
GTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCTAATCGGCTGTCTAGGGT  
GATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAGCAGGATTCTTGGTAAAA  
[C, T]  
TGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGGATT  
TCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG  
CCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCAACA  
GCGGGAGGAGGCGCCGGTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGGGG  
GGCCCCGTGTGGGTGCGCCCAGCGCGTATTGAGTAGAGGGCGAGCCCGTCCCGCCTCT

7398 GAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGG  
GGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTT  
GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCT  
AATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAG  
CAGGATTCTTGGTAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGC  
[T, C]  
TTATTGGGAAGAGGATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCA  
CTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCT  
TGGTGAGAAGGGCAACAGCGGGAGGAGCGCGGTTGCGGAGCGGGAGGCCGGGGGCGGGG  
CTGCGGGGCTGCGGGGCGGGCCCCGTGTGGGTGCGGCCAGCGCGTATTGAGTAGAGGGC  
GAGCCCGTCCCGCCTCTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAAA

7653 AACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGG  
ATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC  
GAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCA  
ACAGCGGGAGGAGCGCCGGTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGG  
GGCGGCCCCGTGTGGGTGCGGCCAGCGCGTATTGAGTAGAGGGCGAGCCCGTCCCGCC  
[T, C]  
CTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAACTCCGCGGGGTCCGC  
GATTTCCCATGGCCGAGCCGCTGCGGCACCAAGGCCATGGCCCTTTCAAGCGCACCTT  
GGTGCTGAGTCCCGCGCGCGGCCAGGGGCCGGGCGCAGGCACCGCCCCGCGGGGCTG  
CTGCTTGCCCTCTGCGCCTGCGCCTGCAAGGACTGGCCTCGGGGAGAGGGCGGCAGGCT  
GTGGAGCCGCTGCCCCAGTCCAGTCCCACTCCCACTCCCACTCCCACTCCCACTCCCTG

8310 CAGCCTGAAAACCTTGCTACAAGTATCTCAATCAGACCAGTCGAGTTTCGCAGCTGTTAT  
CCAGGCGCTGGATGGGGAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGAGGAA  
AGCTTGTCGGGACTTTTGAAGTGTGTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTG  
CAGCCTCGTTGCTGTGGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAA  
GCCCTTCCAGGCTTTTGCCATCTAGTAGAGTCCCTGCGGGCCAGCCTTTAGAGAAAG  
[A, G]  
GGGGGAGGGGGTGATGTTTATTAACCTTTTTTTAGTCTTGGCAGCTGAACCTGCCTGTGA  
GCAGGTCGTGATTTCTCGGCTTCCCTTATCCAACCTTGCATTTCTATTTCTAGCATATT  
GGGTTGATTCTTTGAAGCTGCCTCTGTGCACATTACACCCATGAACCTTAGACCAGTTGC

FIGURE 3Q



CTTTATGTATGATCGTATTTATACTGAGAAGTTACTGTGTTTTTGGACTTTCTTTTCTAT  
TTGCTACATATTAGTTCGGTCTAAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTG

8145 CAGCCTGAAAACCTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT  
CCAGGCGCTGGATGGGAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGGAGGAA  
AGCTTGTCCGGGAC  
[C, T]  
TTTGAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGT  
GGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCT  
TTGCCATCTAGTAG

8031 CAGCCTGAAAACCTTGCTACA  
[G, A]  
GTATCTCAATCAGACCAGTC

8462 GCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGTGGCTTATCCAGAACAT  
AGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCTTTGCCATCTAGTAGAG  
TCCCTGCGGGCCAGCCTTTCAGAGAAGGGGGGGAGGGGGTGATGTTTATTAACCTTTT  
TTAGTCTTGGCAGCTGAACCTGCCTGTGAGCAGGTCGTGATTTCTCGGCTTCCCTTATC  
CAACTTTGCATTTCTATTTCTAGCATATTGGGTTGATTCTTTTGAAGCTGCCTCTGTGCA  
[G, C]  
ATTACACCCATGAACCTTAGACCAGTTGCCTTTATGTATGATCGTATTTATACTGAGAAGT  
TACTGTGTTTTTTGACTTTCTTTTCTATTTGCTACATATTAGTTCGGTCTAAACGTTTGG  
TCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGGAGTAGTGGTG  
ACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCATGTAAGGAAG  
GAAACTAATGTAACCTTCGTTAAGTATGAAAAGCGTTGGATATCCTTATAGTTCCTTAG

8873 AAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGG  
AGTAGTGGTGACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCA  
TGTAAGGAAGGAAAATAATGTAACCTTCGTTAAGTATGAAAAGCGTTGGATATCCTTAT  
AGTTCTTTAGAGTTAAGGGTGAGATGGGTTTAGAAAGTGCCAGGCACAAGTTATTTTAA  
AATAAAAAATCTTTGGCTGTTTGTTCGAATATATTAATAGTTTTCCCTTTTTTACAGCAA  
[C, T]  
GCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACC  
ATCAGTGTGGAAGAAGGTCCCGCTGTGTACACAACCTTCACTCTTTCTTTTACCAACCA  
GACTGGCGGTTTCATGGAGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACG  
GTGAGTGGGGTTACGCATCTGTCTACGGAAGTGTGTGTTTATAATTGCTAACGTGGTTG  
TCCGGTAGCCTCCATACATGTGGAGAAAGGTAAATAAGCATTCTGAGGGCAGCATAATG

9190 ATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACCATCAGTGTGGAAGA  
AGGTCCCGCTGTGTACACAACCTTCACTCTTTCTTTTACCAACCAGACTGGCGGTTTCATGG  
AGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGC  
ATCTGTCTACGGACTGTTGTGTTTATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATA  
CATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAAACTC  
[C, T]  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
TAATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACTAGGTAATGCT  
CTTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTTCCTGTG  
GGAAGACGCAGTCAAATTTAGTGTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTG

9311 GAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA  
TCTGTCTACGGACTGTTGTGTTTATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATAC  
ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAACTCC  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
[T, -]  
AATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACTAGGTAATGCTC  
TTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTTCCTGTGG  
GAAGACGCAGTCAAATTTAGTGTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTGC  
CGACTGTATGATGCAGCCTACCTGTAACACTGCTGGCCTCTTGACTACCCGGAGCCTGGT  
AGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGCGGTGTCTGTGGCA

FIGURE 3R

9847 CTGGTAGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGGCGGTGTCTGT  
TGGCAGCTAGGGCGAGCCTCTGCCACTTCACCTGTGATCCTGGGCAAGTTCCTTATCTGC  
TTTGTGTCTCCGTCTCCTCGTTTGTAAAGTTAGAGCTGAGAGGATTAATTTGCGACATAT  
AAAGTACTTAGTGCCTGGTACAGGGTAAGTATTCTGTAAGTATTAGCTATTTGGTCTATT  
TTGTTGGAGTAAAGTGGGTTATAGTTAAAATCCTAAGATTTTTTAAAGTCCCTCAAGTTCA  
[T, C]  
GTGGACATCTGCCTAGGTCCTACTATCCTAGAATTTCGCATGTCTTATCACACAAATAACT  
GATTCTTCCATATCTATAAATAAAGGTTTGATTTAGCAAAGTCACATGTTGTGTAATAG  
CTCGAAGAAGCCCTTTTGTCCACAGTTGCCAGAGCTTTTGGAGAACAGTCCTTATGTTA  
TTGAAACAAACCTAATCTGTAGCTGAGTTGGGAGGGAGCTAAGTGGACAGAGAGTCTCC  
ACCCAAACAAAAGAACTTTTGATTCTTGGGCATAATGGGAGCAATATTTAAAAAATAA

10460 AGGAATGTTTGGGGAAGACTCTTGCGGTGCAAAGGCTGTTTCAGATTGCTGAGATCAGAC  
CTTAAGTACCAAAGCCCAAATATAGTACAACATAATACAAATGAGAAGAAAATAGCTGAA  
GAATAATTCGATTTTATACAGTACAATTCAAGAGAAGAAAGAAAATTTATGACGACTAGC  
TGGGTGAGAATTAGAACTGTAACCTTGGGAAGGTCCTGGTGATTTGACTCTCACAGGACA  
CCTGATGACCAGAGGATGGGTTTCTTTGATGGGAAATCTGTGGCGATTATTGATGGGC  
[C, T]  
TCTGAATTCGTCTGAAGCAGAGGAAGTAGTAATACCCCATTTATAATGGAAGTGCATTCT  
CACTTAAAAACAATAATATTCTAGCTGGACCTAGCCTCTAGAAAACAGCCAAATTAC  
ATTTGACTTGAAGTGGATTGATAATAATTAATAAATTTCTGGGCGATGGGATAAATGTGT  
AGGTATTGCTAAGTCAAGGCAGCCCTATCCCTCAGCAGAAGTGAGGGAATATGAAAGTG  
TGTGAATGCTAACATAATTTTGGGGAATATCGCCGTCAGATTTCCAGATGATATTCCAAC

20204 TCTGCCAGTTGCGAAGACTGGGAAAAGCACAGTATTTGGGCAGAGTATACTGTTCCCTCA  
GGTACAGTCACTCACGCCTTTCTTTGGCTAGGAAAGGGAAATCCCTTGACCCCTTGCACT  
TCCTGGATGAGGTGACGTCCTGCCCTGCTTTGGCTCACCCCTCCATGGGCTGCACCCACTG  
TCCAACAGTGCCCAATGAGATGAACAGGTACCTCAGTTGGAATGCAGAAATCACCCAT  
CTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGCTGTTCTACTGGGGCATCTTG  
[G, A]  
AGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGATGTATATCCCCAGTGCCTAGAAT  
GATACTTGTTACATAGGAAGTGCTTGATCCATGTTTGACACAAATGAATCTTTCTCATAAT  
GAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTTACACCCAGCTTTATGTTGAAGCAT  
CTCATTATACATTGGAAGATGAAATGTGTAGTGAGACTTTGAATCTTCTTTGAATCTA  
GAAACATTAGCATTTTATAGACCATTCTATTTTAATATTTATGAAATTTATGAAATAATAA

20362 CCTCCATGGGCTGCACCCACTGTCCAACAGTGCCAATGAGATGAACAGGTACCTCAGT  
TGGAATGCAGAAATCACCCATCTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGC  
TGTTCTTACTGGGGCATCTTGAAGCAACTCTGGGTCTGAGTTTCTGTTTGTGCCCCTGA  
TGTATATCCCCAGTGCTAGAAATGATACTTGTTACATAGGAAGTGCTTGATCCATGTTTG  
CACAAATGAATCTTCTCATAATGAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTA  
[C, A]  
ACCCAGCTTTATGTTGAAGCATCTCATTATACATTGGAAGATGAAATGTGTAGTGAGAC  
TTTGAATCTTCTTTTGAATCTAGAAACATTAGCATTTTATAGACCATTCTATTTTAATATT  
TATGAAATTTATGAAATAATAAGAAACATGAGGCCGGGCTCAGTGGCTTATGCCTGTAAT  
CCCAGCAGTTTGGGAGGCCAGGGCTAGTGGATCATGAGGTGAGGAATTTGAGACCAGCTT  
GGCCAAACATGGTGAAACCCCACTTCTACTAAAAATATAAAAAATTAGCTGGGCGTGGTGGT

21166 TAATTCGCCCATGTTTGCCTTGTGATCTTTGGTGCCATGTCTGTACATATTTTCATGATT  
TCTGTGTTTTTACGGTTTCCATTTAGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAA  
TACCAAACAGTGATTGCCGACATTTGCCGAGAATGGGCATTGGGATGGCAGAGTTTTTG  
GATAAGCATGTGACCTCTGAACAGGAGTGGGACAAGGTTAGTCTCATAAAACAGTGTCTG  
TGTGTGATGTATTAGACAGAGCTGGCAGTCCTCATAGTGAAGCTCAGAACAAGAAAAGTT  
[G, A]  
TCCAGTATTTTTCAGCCCTCTGGTTTACAATTTCATCTGTTTAGGTTGAATGTCTCATCA  
TAAACAGTTTATTCCAGAGTTAATTCCAAACAGCAGCTATGTAGGATATCAGCCAGGCT  
AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG  
ATTAATACTACACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTTTCATAGGA  
ATGGTGTGTTGTGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTAT

21477 TCAGCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCATAACAGTTT

FIGURE 3S

ATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCTAGGAGTAGGG  
TACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAAACTA  
CACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCATTTTTTCATAGGAATGGTGTGTG  
TGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTATTTTAAAGCCA  
[G, A]  
TCAGATTTAGCAGGCAGAGACATTTTCAGACATCTAAAGTGTTGATGTATTTTCATACCTTT  
AACTGTGCTTAAATTAGGATCTCCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGTA  
GGTCCAAGGTCTTGGGCCTCTTAATTTTTCAAACCTCAAACTTGACAGCAGTTATCTTT  
GGAACGTCTGATTTGTGCTTCCTAAGTTAACAGCATACAATGACTGCTAGAAATCAATTT  
CTGCATTTAAGGTGAAGTTAGCCGGTACTATGGTTTACCTGTAATCTCAGCACTTTGGG

22230 GGATTGCTTGAGCCCAAGAGTTGAAGTTGCAGTGAGCCATGATTGTGCCACTGCACTCC  
AACGTGGGTGACAGAGCAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAACTTTCT  
GGCCAAGAACCAGCACTGGTTATGATAGTAACTCATTTTCTGTTGTGCAGATTTATTCAG  
GAACTTAATTTTAGGTTGTTGAATAGAAGTTTGTATCAGATAAAATTGAATTAAAAAA  
ATTTTTTTGGAGACAGGGTCTTGCTGTTATCCAGGCTGGTGTGTAGTGGTGTGATCACGG  
[C, T]  
TCCCGCAGCCTCAACCTCCTGGGCTCAGGTGATCCTCCACCTCAGCCTACCGAGTAGC  
TGTAACATACAGTGATGACACCATACAGGCTCATTTTGTACATTTTGTAGAGAGAG  
GGTTTGTCCATGTTGCCAGGCTAGTCTCAAACCTCTGGCATCAAACAGTCTCCCACTC  
TGGCCTCTCAAATGTTGGGATTACAGGCATGACCAGCAATTATTTCAAGGAGTTATTTT  
TTTTCTTCTACTTTGGGGGAAGATGAATTATATAAGTCTCCATTTTAGGAGTATTTCTAC

22941 AATTTCTGTCTACCTAATTTTCAGCAAGATTTCACTCTTTTCATGTTACTTTTGTCCAGA  
ACAAATTTCAAGTGCTTCTCTTCACCTGTGCATTCTCCCCCTGATTAGTCTCTGGCTT  
TGTATTACTTTTCAGTCAGAGACGACTTTTTTTTTTTGAGACAGGGTCTCACTCTGTCCACC  
CAGACTGGAATGCAGTGGCACAGACAAGGCAGCCTTGACCTTCTGGGCTCAAGCAATCTT  
CCTTGCCCTCAGCCTCCTGAGTAACTGGGACCACAGGCACGTTGCCACCATGCCTGGCTA  
[A, G]  
TTTATTTTAATTTTTATTATTTTTGAGACAGGGTATTGCTCTGTCAACCAGGCTGGAGTG  
TAGTGGCATGATCAAGGCTCACTGCAGCCTTCACCTCCTGTGCTCAAGCAGTCTCTCAC  
CTCAGCCTCCCCATTAGCTGGGACTATAGGTCCACACCACTACACCAGGCTAATTTTTGT  
AATTTTTTGGTAGAGACAGGGTTTCATCGTGTTGCCTAGGCTGGTCTTGAGCTCCTGGGC  
TCAAGCGATTACCTGCCTTAGCCTCCCAGGTGTGAGCCACTACACTCAGCCTTTTAAAA

23963 ATACTACCTAGTTTTGAACTCTTAGCCCTGCCACAGACACGGCAGCCCTTGAACCTTC  
CTGGGTTCAAGCGAGCCTCCTACTTCAGCCCCCTGAGTAACTGGGACCACTGGCCTGTGT  
CACTGTGCCTGGCTAATTTTTTTTTTTCTCACATGGGCAATGTTGGGCAAGTTAAATC  
GACTTCTTTGTGCCTCAGTTTCCTCATCTGAAATGGAGATCATACTGCTATGTACCTGAT  
ACAAATGTTGTGAGGATTGAATGTGCAGAGTTCTTTTTTCTGTTGTGTTGTTTGTGAGA  
[C, T]  
GGAGTCTCACTCTG

25686 CTGAAAAATCCTTTAACTCTTGTGGTTGCGGGTGACAGAAAAACAAGCCAGGCCTCCCC  
AGGCAGCATAAGGGGATGTGGAATAAGGATAGATTGACATGAGTTTGCTTCAGGTAGAC  
TGGCTGACTCCCAGGATTCACACCACGTAATCAGTATATTCAAGCCTTGCTGTCCTTGAT  
TTCTTTTCAGACGGTCTTTCTCAAAGTGGTGGATATGGTAAACCCACGTGCACTAGCTT  
AACAAAAAGTTCTTAGGAATGGCTTTGTTCGGCCTGGCGCAGTGGCTCATGCCTGTAATC  
[A, C]  
CAACAGTTTGAGAGGCCAAGGTGGGCGGATCACCTGAGGCCAGGAGTTCGAGACCAGCCT  
GGCCAAATAGTGAAACCCCGTGTCTTACTAAAAATAAAAAATTAGCCGGGCGTGGTGG  
CAAGGGCTTGTAATCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG  
AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTGCACTCCAGCCTGGGCGACAGAGTG  
AGACTCCCTCTCAAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTA

26018 ACCTGAGGCCAGGAGTTTCGAGACCAGCCTGGCCAACATAGTGAAACCCCGTGTCTTACTAA  
AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCAGCTACCTGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT  
GGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGTACACAGCTGAGTTCTCTGGCCTC  
[A, G]  
CCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAGATTCTGCC

FIGURE 3T

GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTTT  
GCTTTCATAAAAGTGTTTCTGCAGCCAAGTACTTTAAAGTTTTAAAAAGACGGGTGAG

26078 AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCCAGCTACCTGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT  
GGTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC  
ACCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAGAATTCTGC  
[G, A]  
GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTTT  
GCTTTCATAAAAGTGTTTCTGCAGCCAAGTACTTTAAAGTTTTAAAAAGACGGGTGAG  
GCTAAGTGTTGTTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGC

26625 TGTGGTGTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGCCTGAGC  
AACACAGCAAGATACCATCTCTATAAAAAATTGTTAGAAAATGATTCTGCTGAAAGAGCA  
AAAAATAAAATTAAAGAAAGTAGAAAAATAAACTAAATTTAAAAGATTAACTGGGCAT  
GTTGGCATGCACCTGTATTCTTAGGTATTGGGAGGCTAAGGCACAAGGATCCCTTGAGC  
GCAGGAGCTCAAGGTTGGATTGAGTTGTAATCACACCACTGCCTCCAGCCTCGGTGGCA  
[C, G]  
AATGAAACTGTCTCAAGAAAAAAGTGAAGAGGGAACAATATTTGCAATTCATA  
GAGCAGATACAGGTTTCATATTCCTAATATTAATAAAAACTTCTAAAGTTAAGAAAAAG  
GCCAACTGCCCCACAGAAAATGGGCAAGGAGATAAGAACAAGATTGTTACAGGAAGAG  
ACACACAGATGATTATTAATAATCTGAAAAGATGCTGAGTCTTACTCTAAGAAAAATTC  
ACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGTAATCTCAACTCTGGG

27151 TCCTAAGAAAAATTACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGT  
AATCTCAACTGGGAGACCAAGGCAGGAAGATCACTGAAGCCAGGGTATCGAGACCAGC  
CTGGACAACGTAGTGAGACCTTATCTCTTAAACAAAAACAAACAAAAACAAAAA  
AACAGTAAAAATTGGCCGGGCACAGTGACTCCTGCCTATAATCCCAGCACTTTGGGAAGC  
CCAGGTGAGTGGATCACTTGAGGTGAGTGTGAGAACAGCCTGGCCAACATGGCAAAA  
[C, T]  
TCCGTCTCTACTAAATTACAAAAATTAGCCAAGTGTGGTGGCATACTGCTGGTAGGGCCA  
GCTACTTGGGAGGCTGATGTGAGACTCCATTTAAAAAATAAATCAAAAATTAGCTGGG  
TATAGTGGCACACCCCTATAGTTCTCGCTCCTTGGGAGGTTGAGGCAGGAGGATTGCCTG  
AGCCAGGAGTTCAAGGCTGCAGTGAACCATGATCACCACTGCATTCTAGCAGCCTGG  
GAGACAGAGCAAAACCCCTGTCTCAAAACAAACAAACAACAACAAAAACAAAAACACTT

28032 AGGAGCAGAGCCCTGCTCTTCTCACTTACTTTATCTGTAATAAGCATCATTTCTA  
CCACACGGTGGTGTGAATAAAATGAGATGAACCTTAGCATAGAGTGCTTAGTAAAG  
GTTCTGGACATTTCTAGTAGTTGAATCATGCCAATGTGGTCTTAGGTGATTGGCTTCT  
TTTGCTAGCATGTTTTCAGGGCTCCTCCATGCTGGGGCATTGCATCACTGCTTTATTCCT  
TTTTATCGCCTAGTATTATTCCACTGTGTGGATAGACCACATTTATCCATTATCAGTTG  
[G, A]  
AGGATATTTGGGTTCTTCCATTTTTTTTGGCTATGGTGAATAGTACTGTGTACATTTGC  
ATATAAGGTTTTGTGTAGATGTGTGTTTCTTTTTTCTGGGTCTATGCTGAGAAGTGGA  
ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGGAGCTGCCAGACGCTTTTCCAAGGT  
CGCTCCACCATTTTACATTCCCGTCAGCAGTGTGAGAGTCCAGTTTACCAGCACTTGT  
TGTTATCTCTTTTTAACTGTATGTATATATACTTAACATTTTATTTATAATAAATGTACA

28772 AAAATCATCAAGCCGAATCCCAGTGTAGAAATTAAGGTTTTATTTCACTTTCAAGTTA  
TCAGGATCCAGGGAGGTGAATACTTAGAGGATAGACTCAGCTCATTTCCAGCTATG  
CCTTTACAGCATTTCTTACCAGAGTAGGAATATAATGTTAGTCATTATTTAGAGGCTG  
GCCATCTTGAGAAGGTTTACTGTTTGTCTGCAGTACAATTATAACTGTTTTTGTATATT  
GGGTTATTTTTTTTCAAGAGTAGGCCAGTAGCTCTAACAGGAGCCTCTTAGCCTGAATTC  
[G, A]  
TCCAAGTAGTGAGTGTGCACTAGTTGTCCCTCGGGACATGCTCCCCAATACGTAACTC  
ACTTCCAGGTTGCAACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCATGGAGCTTA  
AAATGAACCTTGATCTTCGTGAAAGATGAGTCTGCAGCTAAGAGACTTACTGTATATCAT

FIGURE 3U

AGTGTTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTGACGGAGTCTCACTCTTTCACCC  
AGGCTGGAGTGAATGGCGAGATCTTGACTCACTGCAACCTCCGCCCCCTAGGTTCAAGC

29572 TCATAGTTCCTTATGCACAAAGACCCCTTAATATTGTTTGTAATTTCTCCCCTATGCACAC  
GCTGACCTGTTCCCTAATCTTCTTATCTGTCTAGGTTTGGAGCAGGTATGTTAAGAAGTT  
AGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAATGAACCTTAT  
AACCAATGCACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCA  
GAGTGTGTTAACTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATA  
[C, T]  
GGGGCTAAAGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATA  
TGATTCCCTTAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCC  
TTTGCTTCCAGCCACCAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAAC  
CTTCTTTCCGGATTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCA  
CAGTTAAGTCAAGGTCTTTGGCTTAGATTTATGGGGAGTGTGGGTAAAACCTGGGTGAA

29761 ACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCAGAGTGTGTT  
TAACCTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATACGGGGCTAA  
AGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATATGATTCTT  
TAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCCCTTGTCTC  
CAGCCACCAAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAACCTTCTTTC  
[C, T]  
GGATTTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCAGTAAAGT  
CAAGGTCTTTGGCTTAGATTTATGGGGAGTGTGGGTAAAACCTGGGTGAAGCTGTTATC  
ATTAAAAAGTCTTCATTAAGCACCTAATTACTGCTGTCTCTTTTCTAGACCCGGCATAAA  
AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACTTACACTTTTTAGTTG  
CCTTTACCAAGTATTGCAGATACTACTGCAAATAAGTGAAGAAAGTAACAGCATTAACT

30732 ATTCTGTGTGTTGTTGAGAAAGGGAGGAGTGGGGAAGGTAAAAATCTTGACATACTTTCT  
TCGTGGGTATTTTTCTTGAGCGATTCCATCTTAGTTGATTAGCAGTTAGCAATTGCCCA  
TTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACATCATTTCTTCT  
TTTTTCCCTCTCTTCTGTGTCTCTAGGTGATGGCCATTGCCACTTTGGCTGCCTGTTA  
TAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAAGCAGTGACCTT  
[G, C]  
ATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAGTATATGGAAGAG  
GTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGATTAGTAATGTCA  
CTGTTTAAACAGGTTTGGATATTAGATGATCCTAACCAATTCATATCCTGTGGCCTAAAG  
AGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGCCGAGCAGATTG  
CTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCTGTAGGTTGGAG

30841 GCAATTGCCCATTC AACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACA  
TCATTTCTTCTTTTTTCCCTCTCTTCTGTGTCTCTAGGTGATGGCCATTGCCACTTTG  
GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAA  
GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG  
TATATGGAAGAGGTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGAT  
[G, T]  
TAGTAATGTCACTGTTTAAACAGGTTTGGATATTAGATGATCCTAACCAATTCATATCCT  
GTGGCCTAAAGAGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGC  
CGAGCAGATTGCTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCT  
GTAGGTTGGAGCCCTCAGTAGAATCATAGATTTTGTAGCTGCAAGATGATGCAGGAGGCC  
AACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTGATGCAG

31376 GAGGCCAACCAAGCTTCTTGTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTG  
ATGAGTGCGTGATTGAGTGGATCTCTGGCTCCCGTCCATGTGTCTTGACACCCAGTCTG  
GTACTTTTATTATGCCACAGGCCCTCAATTGAAAAATCACAGTAGGGAATTTAGGCCAAGG  
AAAGCCATCAAGTTGCAATTATTTCTAAATTTTCTTGGAAAAATTCATTTCAAATACC  
AAAACCATCCTATAAAAAAGAAAACCTTACCTTCTTAGGTCAAATCTCTAATATTTGACTAG  
[G, A]  
TTCAAAAAGTTTTATTTCTGGCCAGGCACAGTAGCTTACTCTGAAATCCCAGCACTTTGG  
GAGACCAAGGTGGGAGGATCACTTGAAGCCAGGAATTCAGACCCAGCCGGGCGACATAG  
CAAGACCCCATTTCTACAAAAAATTTAAAAATTTGTCATGGTGGTGCACGCCTGTGTGCC  
AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTGAGGCTACAGTA  
AGCTGTGTGATTTTCATCATTGCACTCTAGCCTGGGTGATAGAGTGAGACTTTGTCTCAA

FIGURE 3V

32032 TCTCTAGGCCCTAGAGCAGTGGTTTGTAAATGGAGGTGATTTGCTCCCCCTCCCCCAGAG  
GACATTGGACAATGTCTGGAGACATTTTTGATTGTCTTAACCGGCAGGAATCGGGTGCTA  
CTGGCATCTGGTGAGTAGAGGCCAGGATGATGCTGTGATCCTCAGGTGTGATCCTGTTG  
AGAATGAAACACTGTAGACTTTATGAAAACATACAAGACCCTCATCATTTTTCTTTGCC  
TGAGCTCCCTCCCCAGAGGTTACCTCTGTTTCATGTTTGTGTCATCCGTCTAGTCCCCCT  
[A, G]  
TTACGCGTTTTACAGGAATATGGTTTGCAACAGTGTTTTCATCTAAATAGAATTATACAAA  
ATAGCGATTTCTGATTTCTCTTGTCATATTGCACATTCTTCTTATACTTCTCCCTACCTT  
TATCTGACACAGAAATGCTGTATGTCCAGAATTCTATCAGAGGCACCTATGGAAGTCTA  
AGGGAAGACCACATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATT  
CAGCCAGTGACCCAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAA

32525 ATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATTCAGCCAGTGACC  
CAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAACTTACTTTGATC  
TATGTGCCTGGGTAGTGACCAAGTAGGTGGGTAGGAGTAATCTCAGGGAAACTTGAGGC  
CCAGCCTCATGGCTAGGGTCATAATTTGAACCCAGGTCTGTCTGACATCAGAATCCATG  
ATGTTAAACCCCAATTCTAAGGGGTTCAACTACCCTTTCTAAATGGAATCCTGCTATATTA  
[A, G]  
GCACTATTTATTCATTTTATATAAACTAGAAACATTTTATGTAGTAAGTAGTTGAGAGTG  
TTTTGGTTTTGTCAGTTTGATCACTAGTTTTAGAAACAGTTTTTAAACACTTTGTGGCCA  
ATTCATTACTATATTAATAATTCAGATTTATTTGGTTTTTCTTAACTATTGGGATTAAA  
TCTGTGTTGTAATTCATAGTTTGAAGGCGAGGGTGGCAGTCTACATTTGGCTGAGCCCT  
GTTTTTGTGAATAAATGTTATCAGAACACAGCCACACCCATTGCTTCTATGTCTTCTGT

34179 CTGCTGTATGTAGCACAGCATTGCACAAGAGCTTATTTTCAGTCTAGTAAACATTTATAGG  
AGCCTGTGTCAATTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAACT  
TTGGGAGGCTGAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAAT  
ATGGCAAAACCCCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACT  
TGTCATCCAGCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAG  
[G, T]  
TTGTAGTGAGCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTT  
TCTCAAACCTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGG  
CTATGACCTGTCTTGAACAAGCAGATGTAACCTCCTTGATTGAGGCTAGTAGGTTTTTAAG  
ACCTGAATAATTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGG  
TTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGT

34249 ATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAACTTTGGGAGGCT  
GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAATATGGCAAAAC  
CCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACTTGTATCCCA  
GCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAGGTTGTAGTGA  
GCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACCT  
[T, C]  
CTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTG  
TCCTTGACAAGCAGATGTAACCTCCTTGATTGAGGCTAGTAGGTTTTTAAGACCTGAATAA  
TTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAG  
CAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGT  
CTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGA

34451 GAGCATCGCTTGAACCTCGGAGGTGGAGGTTGTAGTGAGCTGAGATGGCACCCTGCACT  
CCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACCTCCTCAAGTATTTGGCTTCAACT  
TTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTGTCTTGACAAGCAGATGTAAC  
TCCTTGATTGAGGCTAGTAGGTTTTTAAGACCTGAATAATTGAGTTTGCAGAAACCTACT  
GTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTC  
[T, C]  
CTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGCTCTGAGTACCAGTGACTGCAGCT  
CTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTT  
TGCCACTAATTGTATTACCGGGGACTGTCACAACCAAGATTTCTCTAATTTATTCACCT  
TACTTATCTCCTGGAAGGGCATATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTTTGT  
TGGTTGTGTATATCACTTGGGTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCC

34532 AGGCCCTTTCTCAAACCTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGA

FIGURE 3W

AAAGTCGGCTATGACCTGTCTCTTGACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGG  
TTTTTAAGACCTGAATAATTGAGTTTGCAGAACTACTGTGTGCCTTCAGGTAATGGA  
GAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTG  
TTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTCATG  
[T, C]  
TTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTTGGCCACTAATTGTATTACCGG  
GGACTGTCAACAACCAAGATTTCTCTTAATTTATTACCTTACTTATCTCCTGGAAGGGCA  
TATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTGTGTGGTTGTGTATATTCACTTGG  
GTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCCCAAAGGATGTAAGATGGCTT  
ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAAGTAAATGAAGAAA

36541 GGTAGGAGCCAGTTGAAGGGACGTGGGAGGCGCATTCCAGAGAGAAGGAGTGGTATGAGA  
CTGGAACAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTT  
TGTTTTTGTGTTTTTTTGGAGACAGGGTCTTGTCTGTCTATCCAGGCTGGAGTGCAGTGG  
CATGATCTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGT  
CCCCAAGTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATT  
[T, C]  
TGTAAGAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAG  
TCTACATGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCC  
CGGCAACTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGG  
TGCAGTAGGTCTGGACCATGGGTGGCCTTGCCTACACATTACAGAGCTCAGGCTTTTTT  
TCTCCAGGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGG

36607 CAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTTTGT  
TGTTTGTGTTTTTGGAGACAGGGTCTTGTCTGTCTATCCAGGCTGGAGTGCAGTGGCATGAT  
CTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGTCCCCAA  
GTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATTTTGTAG  
AAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTAC  
[A, G]  
TGCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCCGCA  
CTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGT  
AGGTCTGGACCATGGGTGGCCTTGCCTACACATTACAGAGCTCAGGCTTTTTTCTCCA  
GGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAG  
TGTAAGACAGACAGGTAGATTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATA

36681 GACAGGGTCTTGTCTGTCTATCCAGGCTGGAGTGCAGTGGCATGATCTCGGATCACTGCA  
ACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGTCCCCAAGTAGCTGGGGGACC  
ACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATTTTGTAGAAACAGGGTTTTAC  
TGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTACATGCCTCAGCCTCC  
TGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCCGCAACTGTTACTAGACT  
[A, G]  
TAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGTAGGTCTGGACCATG  
GGTGCCCTTGCCTACACATTACAGAGCTCAGGCTTTTTTCTCCAGGTGAGAGGGCTGG  
TGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAGTGTAGAGCAGACAG  
GTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG  
CACTCAGGGCCTAATCTCAGGCAGTAATTTTAGGGATGTAGGGGAAGAGATGGATTCTGC

37493 TGACGTTTATTGGGCCTGGCACTGTGAGGTGCTGGGGATGTGAAGATCATTGTGGCTCAG  
CCGCTGCTCTCGAGGGCCTCTGGGTGCAGTATGCACACCTGTGCCTCCTGTTTGCTCAGG  
AAGACAGGCTTTGAGATGAGCTGGGGCTGACATCCCCACCTTATCATTGGGATGGCTTTG  
GGTAAGTTATGTTTCATGTTCTCTGAGCCTCCCTTTCTCATTGGTAAAATGGGTATAAAA  
TACCTGCCAGTGGAGGGTTGTTGTAAGTAGCCATGGAATGTAAAGCACATAGCACTTA  
[C, T]  
CATTTTTTCTGTGTCTTTAAACAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCT  
AGCAAAACAAGGCAGATCATCTCCACCATCCGGACGCAGAATCTTCCCACTGTGAGCTG  
ATTTCCCGAAGCCACTACTCCCCATCTACCTGTCTGTTTGTGATGCTTTTGGCTGCCCTG  
AGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTACAGCTGGAGAA  
CACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTCT

37966 CTGCCCTGAGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCA  
CTGGAGAACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACT  
TTTTTCTTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCT

FIGURE 3X

AAAAGAACGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAA  
ACATGAAAGGAAAGGTCCTCATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTG  
[C, A]  
TGCTTGTGGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGT  
GACTGTCATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATAAAAGTATTTAA  
TTTGAAGCACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTC  
GGCTCCTATTTTTCTCATCATTTTGTTCCTTTAATTGGGTTGAATGGAGTAGATAGAAA  
TATTTATGGTTTAGGTAACAGTTAGATGTTTCCTAAGAATGCAAACTGCCTTTTCCACAC

37973 GAGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTCACTGGAGA  
ACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACTTTTTTTC  
TTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCTAAAAGAA  
CGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAA  
AGGAAAGGTCCTCATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTG  
[T, C]  
GGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTC  
ATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATAAAAGTATTTAATTTGAAG  
CACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTCCGCTCCT  
ATTTTCTCATCATTTTGTTCCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTAT  
GGTTTAGGTAACAGTTAGATGTTTCCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCT

38113 TCTCTTTATTTTTTCTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTT  
TAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGTCCTCATCCC  
AGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGAGCATT  
AGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTAT  
GATCCTGGCTAGAATGATAATAAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTA  
[C, A]  
TAGTAGAAAATGATGTGAATTTCTTTCTGTTCCGCTCCTATTTTTCTCATCATTTTGT  
TTCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGAT  
GTTTCCCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATCTGGGTAT  
TCTCGTATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGA  
CCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAA

38298 CACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTATGATCC  
TGGCTAGAATGATAATAAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTACTAGT  
AGAAAATGATGTGAATTTCTTTCTGTTCCGCTCCTATTTTTCTCATCATTTTGTTCCT  
TTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGATGTTT  
CCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATCTGGGTATTCTC  
[G, C]  
TATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGACCTTT  
TAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAATTTAA  
TTGCTCTGCATTTGTCAAGTACAGTTCGCTTGAAAGCCTGCCTGACTGTGGAAAAGATGG  
AGCTCAAGAATGGAGTTGATGGCCAGCGTGGTGGCTCATGCCTGTAATCCCAGCACTT  
GGGAGGCTGAGGCGGTCGGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG

FIGURE 3Y